

FIGURE 1

AGGCAGGGCAGCAGCTGCAGGCTGACCTTGAGCTTGGCGGAATGGACTGGCCTCACAAACTGCTGTTCTT
CTTACCATTCATCTCCCTGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGAGGAAGGGCAAGGGCG
GCCTGGGCCCTGGCCCTGGCCCTCACAGGTGCCACTGGACCTGGTGTACGGATGAAACCGTATGCC
GCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCAG
AGAAAGTGTGAGGTCAACTTGAGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGCTACAGCAT
CAACCACGACCCAGCCGTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGCTGTGAACC
CCTTCACCATGCAGGAGGACCGCAGCATGGTAGCGTGCCGGTGTTCAGCCAGGTTCCGTGCGCCGCCGC
CTCTGCCGCCACCGCCCCCACAGGGCCTGCCGCCAGCGCGAGTCATGGAGACCATCGCTGTGGCTG
CACCTGCATCTTAATCACCTGGCCAGAAGCCAGGCCAGCAGCCGAGACCACCTCCTGCACCTT
GTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTGAAAGCAAG

FIGURE 2

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRGPLAPGPHQVPLDLVSRMKPYARMEYERNIEEMVA
QLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVVDLPEARCLCLGCVNPFTMQEDRSMSVVP
VFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

FIGURE 3

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCC
TGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCACAGTCAC
GGTACCCCACACTGCTACTCGGCTGAGGAACGTGCCCTCGGCCAGGGCCCCCACACCTGCTGGCTGAGG
TGCCAAGTGGGGCAGGCTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGAGGC
ACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCCGCCGGAGGAGGTGTTGGAGGCAGACACCCAC
CAGCGCTCCATCTCACCTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTT
CGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGAGACAGCTGCGCTCAACTCCGTGC
GGCTGCTCCAGGCCTGCTGGTGTGCCGCCCTGCTCCCGCGACGGCTGGGCTCCCCACACCT
GGGGCCTTGCCTTCCACACCGAGTTACCCACGTCCCCGTGGCTGCACCTGCGTGTGCTGCCCGTTCAAGT
GTGACCGCCGAGGCCGTGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCATTATGTG
TATTTATTGTTATTATGCCTCCCCAACACTACCCCTGGGTCTGGCATTCCCGTGTCTGGAGGAC
AGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGTAGAAGGAGCTCAGCACCTCTCCAGC
CCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCGTACCTTGGCTCCCTGCTCCGGCTTCCCT
TACCCCTATCACTGGCCTCAGGCCCGCAGGCTGCCTTCCAACCTCCTGGAAGTACCCCTGTTCTTA
AACAAATTATTTAAGTGTACGTGTATTATTAAACTGATGAACACATCCCCAAAA

FIGURE 4

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPPLLARGAKWGQALPVALVSSLE
AASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLRGCIDARTGRE
TAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV

Signal peptide:	Amino acids 1-18
Tyrosine kinase phosphorylation site:	Amino acids 112-121
N-myristoylation sites:	Amino acids 32-38;55-61;133-139
Leucine zipper pattern:	Amino acids 3-25
Homologous region to IL-17:	Amino acids 99-195

FIGURE 5

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGTTCCACGAGGCCTGTCAGTCA
GTGCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTAGTCAGTGAGAGGGCTGCCTGAGGGCT
GTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCAAGCTGCCAGGTTGGGCTGG
GGGCCAAGTGGAGTGAGAAACTGGGATCCCAGGGGGAGGGTGCAGATGAGGGAGCGACCCAGATTAGGTGA
GGACAGTTCTCTCATTAGCCTTTCTACAGGTGGTGCATTCTGGCAATGGTCATGGGAACCCACACCT
ACAGCCAATGGCCCCAGCTGCTGCCCAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT
GTGCCTGTGCCTCCCTAGAGCCTGCTAGGCCAACGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGA
CCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCAGGA
CCTGTACCACGCCGTTGCCGTGCCCCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGG
GCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACAGGCCAGGCTGCCATGGCGAGAAGGGCACC
CACAAAGGGCTACTGCCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGCGGCCCGTGT
GATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTGGAAACCTGGAGCCAGGTGTACAACCACCTG
CCATGAAGGGCCAGGATGCCAGATGCTTGGCCCTGTGAAGTGCTGTGGAGCAGCAGGATCCCCGGAC
AGGATGGGGGGCTTGGGAAAACCTGCACATTTCAGAAAAGAGCAGCTGCTTAGGCCGC
CGGAAGCTGGTGTCCGTCACTTCTCTCAGGAAAGGTTCAAAGTTCTGCCATTCTGGAGGCCACCA
CTCCTGTCTCTCCCTTTCCATCCCTGCTACCCGCCAGCACAGGCACTTCTAGATATCCCC
CTTGCTGGAGAAGAAAGAGCCCTGGTTTATTGTTACTCATCACTCAGTGAGCATCTACTTGG
GTGCATTCTAGTGTAGTTACTAGTCTTGTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATA
GAGATTATCCAAATAAATCTTATTAAAAATGAAAAA

FIGURE 6

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPKGQDTSEELLRWSTVPVPPLEPARPNRHP
ESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSELLYHNQTVFYR
RPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Signal peptide: Amino acids 1-32

N-glycosylation site: Amino acids 136-140

Tyrosine kinase phosphorylation site: Amino acids 127-135

N-myristoylation sites: Amino acids 44-50;150-156

FIGURE 7

**ATGCTGGTAGCCGGCTCCTGCTGGCGCTGCCGCCAGCTGGCCGGCCCCAGGGCGGGCAGGCG
CCCCCGCGGGCGCGGGCTGCGCGACCGCCGGAGGAGCTACTGGAGCAGCTGTACGGCGCCTGGCG
CCGGCGTCTAGTGCCTTCACCACACGCTGCAGCTGGGCCGCGTGAAGCAGCGCAACCGAGCTGC
CCGGCAGGGGCAGGCCGGCGACCGCCGCTCCGGCCGCCACCAACCTGCGCAGCGTGTGCCCTGGC
CTACAGAATCTCCTACGACCCGGCGAGGTACCCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGCT
GCCTGACCGGGCTGTTGGCGAGGAGGACGTGCGCTTCCGCAGCGCCCTGTCTACATGCCAACCGTC
CTGCGCCGCACCCCCCGCTGCGCCGGCGCTCCGTCTACACCGAGGCCTACGTACCATCCCCGTGG
CTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACA
AAACAGGGCGCCAAGCTCCTGCTGGCCCCAACGACGCCCGCTGGCCCTGAGGCCGGTCTGCCCGGGAGGTCT
CCCGCATCCCAGGGGCCAACGCTGGAGGCCCTGGAGGGCTCGTCCGACCTCTGAAGAGAGTGCACC
GAGCAAACCAAGTGCAGGAGCACAGCGCCGCTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGG
GCATCCCTGGCTTGTCTTCTAGCTACAAGCAAGCAGCGTGGCTGGAGCTGATGGAAACGACCCGGCACGG
GCATCCTGTGTGCGGCCCGCATGGAGGGTTGGAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATC
GGCTGCTGCCGGTGCAGGGCGTGAECTACCGCTGGTGCTTGCAAAGAGATAGGGACGCATATGCTTTT
AAAGCAATCTAAAATAATAAGTATAGCGACTATATACCTACTTTAAAATCAACTGTTTGAATAGA
GGCAGAGCTATTTATATTATCAAATGAGAGCTACTCTGTTACATTCTAACATATAACATCGTTTTT
ACTTCTCTGGTAGAATTAAAGCATAATTGGAATCCTTGATAAATTGTTAGCTGGTACACTCTGG
CCTGGGTCTCTGAATTCAAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGTCTCATCTGACCCACTC
TTCCTTCACTGAAGGTCTCACGGCCTCCAGGTGGACCAAAGGGATGCACAGGGCGCTCGCATGCCCA
GGGCCAGCTAAGAGTTCCAAAGATCTCAGATTGGTTTAGTCATGAATAACATAAAACAGTCTCAAACCTCGC
ACAATTTTTCCCCCTTTGAAAGCCACTGGGCCAATTGTTAGAGGTTAGGAGATAAGAAGTGG
ACGTGACATCTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGAAGGGCTTGGATCA
GGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGAGAGATCAATCTGGAGGCTCTGTTCTGCA
TTCTGCCACGAGAGCTAGGTCTTGATCTTTCTTAGATTGAAAGTCTGTCTGAACACAATTATTGT
AAAAGTTAGTAGTTCTTTAAATCATTAAAGAGGCTTGCTGAAGGAT**

FIGURE 8

MLVAGFLLALPPSWAAGAPRAGRRPARPRGCADRPEELLEQLYGRILAAGVLSAFHHTLQLGPREQARNASC
PAGGRPGDRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVFRSAPVYMPTVV
LRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGAKLLLGPNDAPAGP

Signal peptide: Amino acids 1-15

N-glycosylation sites: Amino acids 68-72;181-185

Tyrosine kinase phosphorylation site: Amino acids 97-106

N-myristoylation sites: Amino acids 17-23;49-55;74-80;
118-124

Amidation site: Amino acids 21-25

FIGURE 9

CAACTGCACCTCGTTCTATCGATAGCCACCAGCGCAACATGACAGTGAAGACCCCTGCATGGCCCAGCCAT
GGTCAAGTACTTGCTGCTGTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCA
AAGTAGGACATACTTTTCCAAAAGCCTGAGAGTTGCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGAC
ATTGGCATCATCAATGAAAACCAGCGCGTTCCATGTCACGTAACATCGAGAGCCGCTCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCAGTGTAGGAACCTGG
GCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCATCCAGCAAGAGACCCCTGGTCGTC
CGGAGGAAGCACCAAGGCTGCTCTGTTCTTCCAGTTGGAGAAGGTGCTGGTGAUTGTTGGCTGCACCTG
CGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCCACTCAGCTGAAGAAG

FIGURE 10

MTVKTLHGPAMVKYLLLSILGLAFLSEAAARKIPKGHTFFQKPESCPPPGGSMKLDIGIINENQRVSMS
RNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSVSFQ
LEKVLVTVGCTCVTPVIHHVQ

Signal sequence: Amino acids 1-30

N-glycosylation site: Amino acids 83-86

N-myristoylation sites: Amino acids 106-111;136-141

FIGURE 11

CGGGCGATGTCGCTCGTGTGCTAACGCCTGGCCGCGCTGTGCAAGGAGCGCCGTACCCCGAGAGGCCGACCGT
TCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGACTTGA
GGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGACTATTCAATTGATGAATGTAAGC
TGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAAGATTGTGTGACGGGCAAAGCAA
CTTCCAGTCCTACAGCTGTGAGGTGCAATTACACAGAGGCCTCCAGACTCAGACCAGACCCCTGGTG
GTAAATGGACATTTCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTCTATTGGGCCATAAT
ATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCTCACCAGGCTGCCAGA
CCACATAATGAAATATAAAAAAAAGTGTGTCAAGGCCGAAGCCTGGGATCCGAACATCACTGCTTGT
AGAAGAATGAGGAGACAGTAGAAGTGAACCTCACACCCTCCCTGGAAACAGATACTGGCTTTATC
CAACACAGCACTATCATGGGTTTCTCAGGTGTTGAGGCCACACCAGAAGAAACAAACCGCAGCTTCAGT
GGTATTCCAGTGACTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTCCTACTTGTGGCA
GCGACTGCATCCGACATAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTCCCTGGATAAC
AACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTGCTGGTGGCCACATGGGTGCTGGT
GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTCCCTTTCTACCACACACTACTGC
CCCCCATTAAGGTTCTGTGGTTACCCATCTGAAATATGTTCCATCACACAATTGTTACTTCAGTGA
TTTCTTCAAAACCATTGCAGAAGTGAGGTATCCTGAAAAGTGGCAGAAAAGAAAATAGCAGAGATGGG
TCCAGTGCAGTGCTTGCCACTCAAAGAAGGAGCAGACAAAGTCGTCTCCTTCCAATGACGTCA
ACAGTGTGTGCGATGGTACCTGTGGCAAGAGCAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTCCCC
CTTGCCTTAACTTTCTGCAGTGATCTAAGAAGCCAGATTCTGCACAAATACGTGGTGGTACTTT
TAGAGAGATTGATACAAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCAACCTCATGAAGGATG
CCACTGCTTCTGTGCAGAACCTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAGATCACAAGCCTGC
CACGATGGCTGCTGCTCCTGTAG

FIGURE 12

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTSVATGDYSILMNVS梧
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDEGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPTVGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVPFPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRCSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSCDGTCGKSEGSPESENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVVKQQVSAGKRSQACHD
GCCSL

Signal sequence:	Amino acids 1-14
Transmembrane domain:	Amino acids 290-309
N-glycosylation sites:	Amino acids 67-70;103-106;156-159; 183-186;197-200;283-286
cAMP- and cGMP-dependent protein kinase phosphorylation sites:	Amino acids 228-231;319-322
N-myristoylation site:	Amino acids 116-121
Amidation site:	Amino acids 488-491

FIGURE 13

ACACTGGCAAACAAAAAGAAGCACTCCGTGCTGGAAGTAGGAGGAGACTAGGACTCCCAGGACAGAG
 AGTGCACAAACTACCCAGCACAGCCCCCTCGCCCCCTGGAGGCTGAAGAGGGATTCCAGCCCCCTGCCA
 CCCACAGACACGGGCTGACTGGGGTGTCTGCCCTGGGGGGGGCAGCACAGGGCTCAGGCCTGGGT
 GCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTGCTGTCCTGGCACTGGCGAAGGCCAGTGG
 TCCTTCTCTGGAGAGGCTGTGGGGCTCAGGACGCTACCCACTGCTCTCCGGGCCTCTCCGTGCCCTC
 TGGGACAGTGACATACTCTGCCTGCCCTGGGACATCGTGCCTGCTCCGGGCCGTGCTGGCGCTACGCA
 CCTGCAGACAGAGCTGGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCC
 ACTTGGCCGTGCATGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTGGAGGAGCAGCTGACTCAGGG
 GTGGAGGAGCCTAGGAATGCCTCTCCAGGCCAAGTCGTGCTCTCCTCAGGCCTACCCACTGCCCG
 CTGCGTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTGTGCAAGTTGGTCAGTCTGTGGCTCTGTGGTATAT
 GACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGCCTATACTCAGCCCAGGTACGAGAACAGGA
 ACTCAACCACACACAGCAGCTGCCCTGCCCTGGCTAACGTGTCAAGCAGATGGTACAACGTGCATC
 TGGTTCTGAATGTCCTGAGGAGCAGCACCTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCA
 AAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTGAACCACACAGACCTGGTTCCCTG
 CCTCTGTATTCAAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACC
 CCCGCGCACACCAGAACCTCTGGCAAGCCGCCACTGCACTGCTGACCTGCAAGAGCTGGCTGCTGGAC
 GCACCGTGCTCGCTGCCCGAGAACGGCACTGTGCTGGGGCTCCGGTGGGGACCCCTGCCAGCCACT
 GGTCCCACCGCTTCTGGAGAACGTCACTGTGACAAGGTTCTCGAGTCCATTGCTGAAAGGCCACC
 CTAACCTCTGTGTTCAAGGTGAAAGCTCGGAGAACGCTGCACTGCAAGGAGTGTGGCTGACTCCCTG
 GGGCCTCTCAAAGACGATGTGCTACTGTTGGAGACACGAGGCCCAAGGACAACAGATCCCTGTGCCCTT
 GGAACCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCACGAGGGCAGCTGCCCTGGAGAGTACTTAC
 TACAAGACCTGCAGTCAGGCCAGTGCTGCACTGCAAGCTGCTGGCTGGCTGGCTGCCCTACTCTTGCCGTGCGCTTTC
 ATGGACAAATACATCCACAAGCGCTGGCCCTCGTGTGGCTGGCTGCCCTACTCTTGCCGTGCGCTTTC
 CCTCATCCTCTTCTCAAAAGGATCACCGAAAGGGTGGCTGAGGCTCTGAAACAGGACGTCCGCTCG
 GGGCGGCCAGGGCCGCCGGCTCTGCTCCTACTCAGCGATGACTCGGTTTCAGGCGCTGGAGCCGTGGTGG
 GGCGCCCTGGCGTGGCCCTGTGCCAGCTGCCGTGCCGTAGACCTGTGGAGCCGTGTA
 GAGCGCGCAGGGGCCGTGGCTGGTTCA CGCGCAGCGGCCAGACCCCTGCAGGAGGGCGCGTGGTGG
 TCTTGCTCTCTCCGGTGCCTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGTGTCCGGGGCCGG
 GCGCACGGCCCGACGACGCCCTCCGCCCTCGCTCAGCTGCCGTGCCGACTTCTGCAAGGGCCGG
 GCCCGGCAGCTACGTGGGGCTGCTCGACAGGCTGCTCACCCGGACGCCGTACCCGCCCTTCCGCA
 CCCTGCCGTCTCACACTGCCCTCCCAACTGCCAGACTTCTGGGGCCCTGCAGCAGCCTCGCGCCCG
 CGTCCGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCAGGGCCCTCAGCCAGCCCTGGATAGCTACTT
 CCATCCCCGGGGACTCCCGCCGGACGCCGGTGGGACCAGGGCGGGACCTGGGGCGGGGACGGGA
 CTTAAATAAAGGCAGACGCTGTTTCTAAAAAA

FIGURE 14

MPVPWFLLSLALGRSPVVLSLERLVPQDATHCSPGLSCLRWDSDLCLPGDIVPAPGPVLAPTHLQTELV
 LRCQKETCDLCLRVAVHLAVGHWEEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV
 QVPAALVQFGQSVGSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSDGDNVHLVLNV
 EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDVRTNICPFREDPRAHQN
 LWQAARLRLTLQSWLDAPCSPLAEAALCWRAPIGGDPCQPLVPPLSWENVTVDKVLEFPPLLKGHPNLCVQ
 VNSSEKLQLQECLWADSLGPLKDDVLLERGPQDNRSCLALEPSGCTSPLSKASTRAARLGLEYLLQDLQS
 GQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLLLLKKDHAKGWLRLLKQDVRSGAAARG
 RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRQTLQEGGVVLLFSP
 GAVALCSEWLQDGVSAGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTPVFT
 LPSQLPDFLGALQQPRAPRGSRQLQERAEQVSRALQPALDSYFHPPGTAPGRGVGPAGPGAGDGT

signal sequence: Amino acids 1-20

transmembrane domain: Amino acids 453-473

N-glycosylation sites: Amino acids 118-121;186-189;198-201;
 211-214;238-241;248-251;334-337;
 357-360;391-394

Glycosaminoglycan attachment site: Amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 Amino acids 552-555

N-myristoylation sites: Amino acids 107-112;152-157;319-324;
 438-443;516-521;612-617;692-697;
 696-701;700-705

FIGURE 15

CGAGGGCTCCTGCTGGTACTGTGTTGCTGCTGCACAGCAAGGCCCTGCCACCCACCTCAGGCCATGCAG
 CCATGTTCCGGGAGCCCTAATTGCACAGAAGCCCATGGGGAGCTCCAGACTGGCAGCCCTGCTCCTGCCTC
 TCCTCCTCATAGTCATCGACCTCTGACTCTGCTGGGATTGGCTTCGCCACCTGCCCACTGGAACACC
 CGCTGTCCTCTGGCCTCCCACACGGATGACAGTTCACTGGAAGTCTGCCATATCCCTGCCACCTG
 GTGGGCCCTCTTCTCCACAAAGCCTTGGTGTGCGAGTCTGGCACTGTTCCCGCTGTTGTGCCAGCATCTGC
 TGTCAGGTGGCTCAGGTCTCAACGGGCCTTCCACCTCTGGTGAGAAATCCAAAAAGTCTTCACA
 TTCAAGTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCCTGTCACCTGTC
 TGAGAAGAGCCATCACATTCCATCCCCCTCCCCAGACATCTCCCACAAGGGACTTCGCTCTAAAGGACCC
 AACCTCGGATCCAGAGACATGGGAAAGTCTTCCAGATTGGACTCACAAAGGCATGGAGGACCCGAGTTC
 TCCTTGTGATTGCTGCCCTGAGGCCGGCTATTGGGTGACCATATCTCAGGCCCTGAGGTCAAGCGTGC
 TCTTGTCAACCAGTGGCACTGGAGTGTGAAGAGCTGAGCAGTCCCTATGATGTCAGAAAATTGTGTCTG
 GGGGCCACACTGTAGAGCTGCCCTATGAATTCTTCTGCCCTGTCTGTGCATAGAGGCATCCTACCTGCAA
 GAGGACACTGTGAGGCAGAAAAATGTCCCTCCAGAGCTGGCCAGAACCTATGGCTGGACTTCTGGAA
 GTCAGTGCACTTCACTGACTACAGCCAGCACACTCAGATGGTCATGCCCTGACACTCCGCTGCCCACTGA
 AGCTGGAAGCTGCCCTGCCAGAGGCACGACTGGCATACCCCTTGCAAAGACCTCCGAATGCCACGGCT
 CGAGAGTCAGATGGGTGGTATGTTTGGAGAAGGTGGACCTGCACCCCCAGCTCTGCTCAAGTTCTTT
 TGGAAACAGCAGCCATGTTGAATGCCCTCACAGACTGGGTCTCTCACATCCTGGAATGTAAGCATGGATA
 CCCAAGCCCAGCAGCTGATTCTCACTTCTCAAGAATGCATGCCACCTTCAGTGCTGCCCTGGAGGCC
 CCAGGCTGGGGCAGGACACTTGGTGCACCCCCCGTGTACACTGTCAGCCAGGCCGGGCTCAAGCCCAGT
 GTCACTAGACCTCATCATTCCCTCCTGAGGCCAGGGTGCTGTCTGGTGTGGCGGTCAAGATGTCCAGT
 TTGCCCTGGAAGCACCTCTTGTGTCAGATGTCCTTACAGACACCTGGGCTCTTGATCCTGGCACTGCTG
 GCCCTCCTCACCCACTGGGTGTTCTGCCCTCACCTGCCGGCCACAGTCAGGCCGGGCCAG
 GCAGGCCAGTGCTCCTCCTGCACGCCGGACTCGGAGGCCAGCGGCCCTGGTGGGAGGCCGTGGCTGAAC
 TGCTACGGGCAGCGCTGGCGCGGGCGACGTGATGTGGACCTGTGGAGGGAGGCCAGTGCGCGCG
 GGGCCCGCTGCCGTGGCTCTGGCGCGCGACGCCGTAGCGCGGGAGCAGGCCACTGTGCTGCTG
 GGAGCGCGCCGACCTTCGCCCGGTCAAGCGGCCCGACCCCCCGGCCGCCCTGCTGCCCTGCTCCAC
 GCTGCCCGCGCCCGTGTGCTGCTGCTTACCTCAGTCGCCCTGCGCCAAGGGCGACATCCCCCGCC
 GCTGCCGCCCTGCCGCGTACCGCCTGCTGCCGCGACCTGCCGCGTGTGCTGCCGCCCTGGACGCCGG
 CTTTCCGAGAGGCCACCAGCTGGGCCCTGGGCCGGCAGGCCAGGCCCTAGAGCTGTGC
 AGCCGGCTTGAACGAGAGGCCCGACTTGCAAGACCTAGGTTGAGCAGAGCTCCACCGCAGTCCCGGGTGTCT

FIGURE 16

MGSSRLAALLLPLLLIVIDLSDSAGIGFRHLPWNTRCPLASHTDDSF TGSSAYIPCRTWWALFSTKPWCVRVWHCSRCLCQHLLSGGSGLQRGLFHLLVQKSKKSTFKFYRRHKMPAPAQRKLLPRRHLSEKSHHISI PPDISHKGLRSKRTQPSDPETWESLPRLDQRHGGEFSFDLLPEARAIRVTI SSGPEVS VRLCHQWALECEELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQS WPEAYGSDFWKSVHFTDYSQH TQMVMALTLRCPLKLEAACRHDWHTLC KDL PNATARESDGWYVLEKVDLHPQLCFKFSFGNSSHVECPH QTGSLT SWNVSM DTQAQQ LILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDIIIPFLR PGCCV LVWRS DVQFAWKHLLCPDVSYRHLGLL LALL ALLTLLGVVLALT CRRPQSGPGPARPVLLHAAD SEAQRRLVGALAE LLRAALGGGRDVIVDLWEGRHVARVGPLWLWAARTRVAREQGTVLLLW SGADLRPVS GPD PRAAPLL ALLHAAPRPLL LAYFSRLCAKGDI P PPLRALPRYRLLRDL P RLLRALDARPFAEATSWGR LGARQR RQSRLE LCS RLERAARLADLG

Signal peptide:	Amino acids 1-23
Transmembrane domain:	Amino acids 455-472
N-glycosylation sites:	Amino acids 318-322; 347-351; 364-368
Glycosaminoglycan attachment site:	Amino acids 482-486
cAMP- and cGMP-dependent protein kinase phosphorylation sites:	Amino acids 104-108; 645-649
Tyrosine kinase phosphorylation site:	Amino acids 322-329
N-myristoylation sites:	Amino acids 90-96; 358-364; 470-476
Eukaryotic cobalamin-binding proteins:	Amino acids 453-462

FIGURE 17

GCCAGGCCCTATCTCCCTGCCAGGAGGCCGGAGTGGGGGAGGTCAAGACGGGGCGGTTGGAGGGGAGGGGG
GCCACCGCGCTCTGCCTCAGGTGTTCTGCCTGCGTTGTCAGTGGAGAGCAGGGAGTGGGGCCAGCCAGCA
GAAACAGTGGGCTGTACAACATCACCTCAAATATGACAATTGTACCACCTACTGAATCCAGTGGGAAG
CATGTGATTGCTGACGCCAGAATATCACCATCAGCCAGTATGCTTGCCTGACCAAGTGGCAGTCACCAT
TCTTTGGTCCCAGGGCCCTCGGCATCGAATTCCCTGAAAGGATTCGGGTAATACTGGAGGAGCTGAAGT
CGGAGGGAAAGACAGTCCAACAACTGATTCTAAAGGATCGAACGCTAACAGTAGCTCAAAGAAG
GGAATGGAATCTCAACCTTCCTGAATATGAAATTGAAACGGATTATTCGTAAAGGTTGTCCCTTTCC
TTCCATTAAAAACGAAAGCAATTACCACCCCTTCTTAGAACCCGAGCCTGTGACCTGTTACAGC
CGGACAATCTAGCTTGAAACCCCTCTGGAAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGC
AGGTGTCCCTCGACCACGCACCGCATGGCTCGGACATGCAGGTGTCCTCGACCACGCACCGACAACCTC
GGCTTCCGTTCTTCTATCTCACTACAAGCTCAAGCACGAAGGACCTTCAAGCGAAAGACCTGTAAGCA
GGAGCAAACATACAGAGATGACCAGCTGCCTCCTTCAAAATGTTCTCAGGGGATTATATAATTGAGCTGG
TGGATGACACTAACACAACAAGAAAAGTGTGATTATGCCCTAAAGCCAGTGCACCTCCCGTGGCCGG
CCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGATTGCGACGCTCTTCACTGTGAT
GTGCCGCAAGAAGCAACAAGAAAATATATTACACATTAGATGAAGAGAGCTGAGTCTTCCACATACA
CTGCAGCACTCCCAAGAGAGAGGCTCGGCCGCGGCCGAAGGTCTTCTCTGCTATTCCAGTAAAGATGGC
CAGAACATGAATGTCGTCAGTGTGTTCGCTACTCCCTCCAGGACTTCTGTTGAGGTGGCT
GGACCTGTGGAAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAGAATGGGTATCCAGAAGATCCACAG
CCCAGTTCATCATTGTGGTTGTTCCAAAGGTATGAAGTACTTGTGGACAAGAAGAACTACAAACACAAA
GGAGGTGGCCGAGGCTCGGGAAAGGAGAGCTCTCCTGGTGGGGTGTCAAGCATTGCCGAAAGCTCCG
CCAGGCCAAGCAGAGTTCGTCGCGCGCTCAGCAAGTTATGCCGTACTTTGATTATCCTGCGAGG
GAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTCCTCAGCTCTGTTCC
CACCTGCACTCCCGAGACCACGCCCTCCAGGAGCCGGGAGCAGCACCGCAGAGGAGCAAGGAAC
CTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCATTGCAACATGCACTGAGGAGTATTGACGAGGAGC
CCGACTGGTTGAAAGCAGTTGCTCCCTCATCCTCCACTGCGCTACCGGGAGCCAGTCTTGGAG
AAATTGATTGGCTTGGTTAAATGATGTCATGTGCAAACCAAGGGCCTGAGAGTGAATTCTGCCCTAAA
GGTAGAGGCGGCTGTTCTGGGCAACCGGACCAGCCACTCCAGCACGAGAGTCAGCATGGGGCCTGG
ACCAAGACGGGGAGGCCCTGCCCTGACGGTAGGCCGCGCCCTGCAACCCCTGTCACACGGTAAA
GCCGGCAGCCCTCGGACATGCCGCGGACTCAGGCATCTATGACTCGTCTGCCCCATCCGAGCTGTC
TCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGAAACGTCTCCCTGACGGAGAGCGTGTCCCT
CTTCAGGCCGGTGGAGGAGGAACCTCCTGCCCTTCCAAGCTCCTCTTCTGGGTATGCAAAGCA
GATCTTGGTTGCCGAGCTACACTGATGAACTCCACGCCGCGCCCTTGTAAACAAACGAAAGAGTCTA
AGCATTGCCACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 18

MPRASASGVPAFLVSGEQGVGPASRNGLYNITFKYDNCTTYLNPGKHVIADAQNITISQYACHDQVAVT
 ILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF
 PSIKNESNYHPFFFTRACDLLLQPDNLACKPFWKPRNLNISQHGSMDMQVSFDHAPHGSDMQVSFDHAPHN
 FGFRFFYLHYKLKHEGPKRKTCQEQTTMSTSLLQNVSPGDYIIELVDDTNTRKVMHYALKPVHSPWA
 GPIRAVAVTVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSSTYTAALPRERLRPRPKVFLCYSSKD
 GQNHNMVVQCFAYFLQDFCGCEVALDWEDFSLCREGQREWVIQKIHESQFIIIVVCSKGKYFVDKKNYKH
 KGGGRGSGKGELFLVAVSAIAEKLQRQAKQSSAALSKFIAVYFDYSCEDVPGILDSTKYRLMDNLPQLC
 SHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVL
 EKFDGVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGLDQDGGEARPALDGSAAALQPLLHTV
 KAGSPSDMPRDGSIYDSSVPSELPLMEGLSTDQTETSSLTESVSSSSGLGEEEPALPSKLLSGSCK
 ADLGCRSYTDELHAVAPL

Transmembrane domain: Amino acids 283-307

N-glycosylation sites: Amino acids 31-34;38-41;56-59;
 113-116;147-150;182-185;266-269

Glycosaminoglycan attachment sites: Amino acids 433-436;689-692

cAMP- and cGMP-dependent protein kinase phosphorylation:
 Amino acids 232-235

Tyrosine kinase phosphorylation sites: Amino acids 312-319;416-424

N-myristoylation site: Amino acids 19-24;375-380;428-433;
 429-434;432-437;517-522;574-579;
 652-657;707-712

FIG. 19

FIG. 20

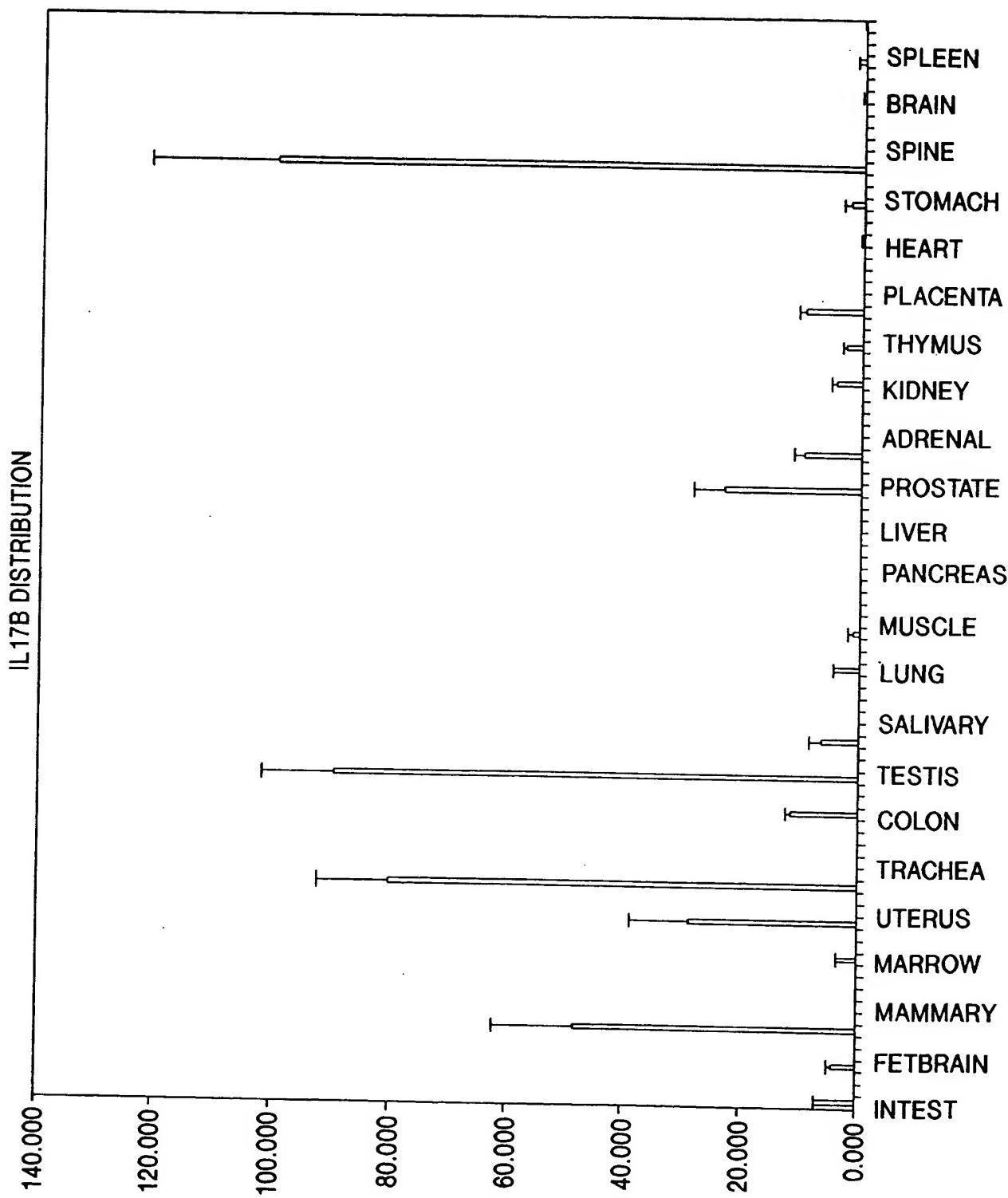


FIG. 21

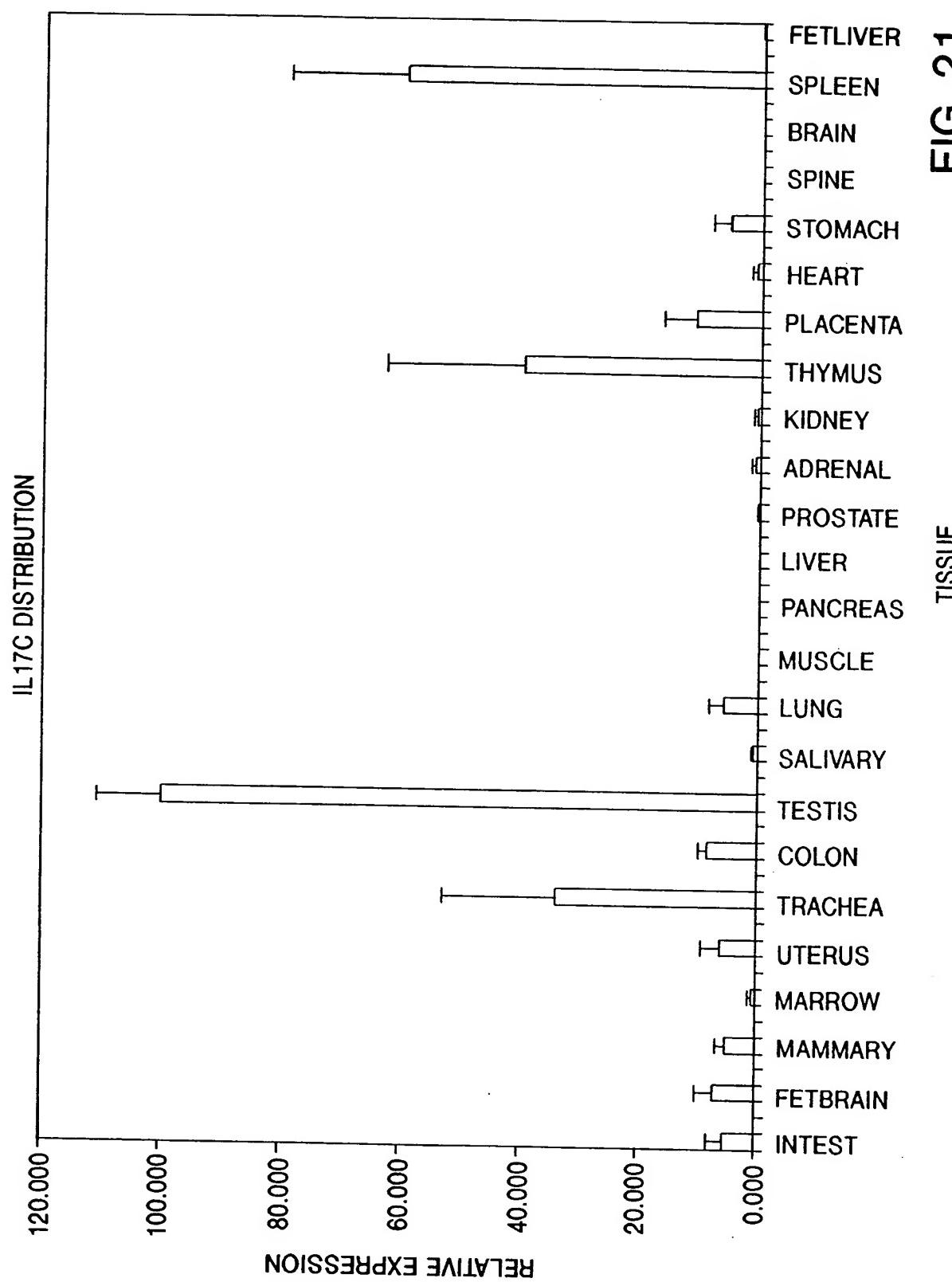
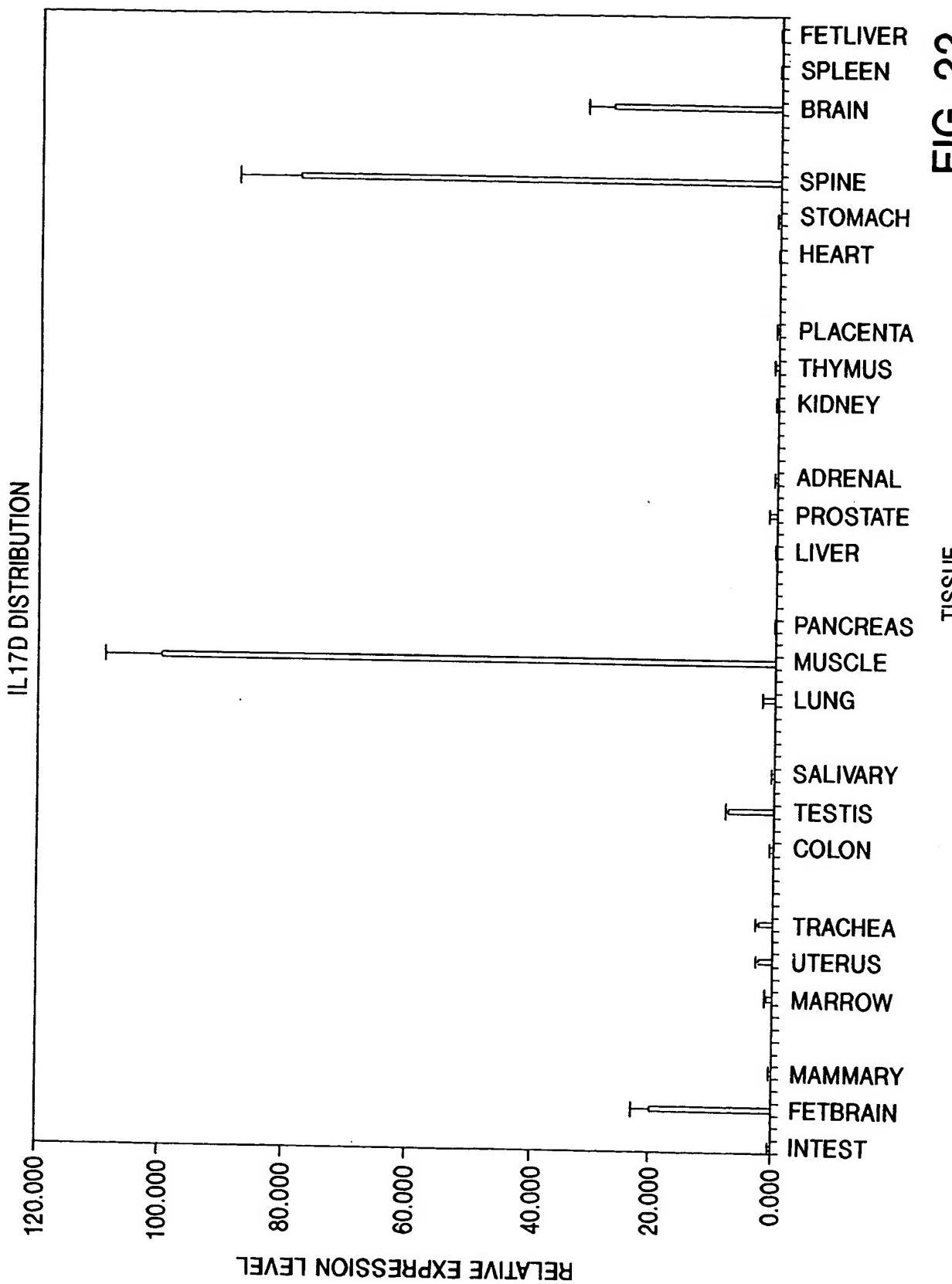


FIG. 22



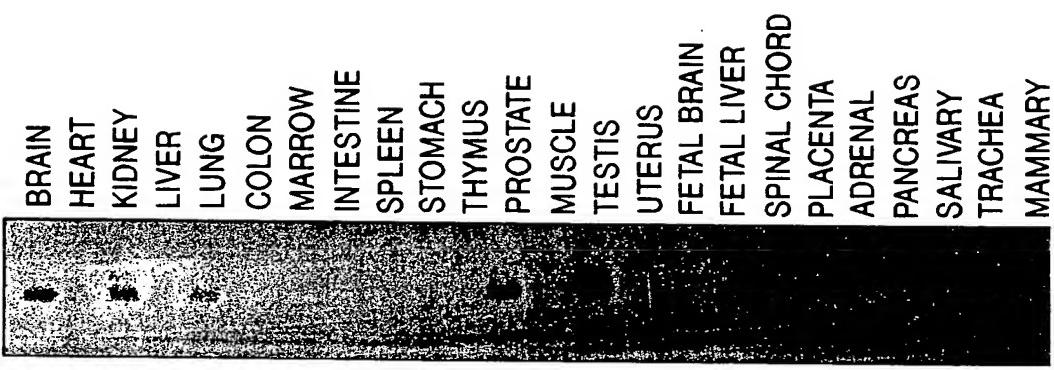


FIG. 23

FIG. 24

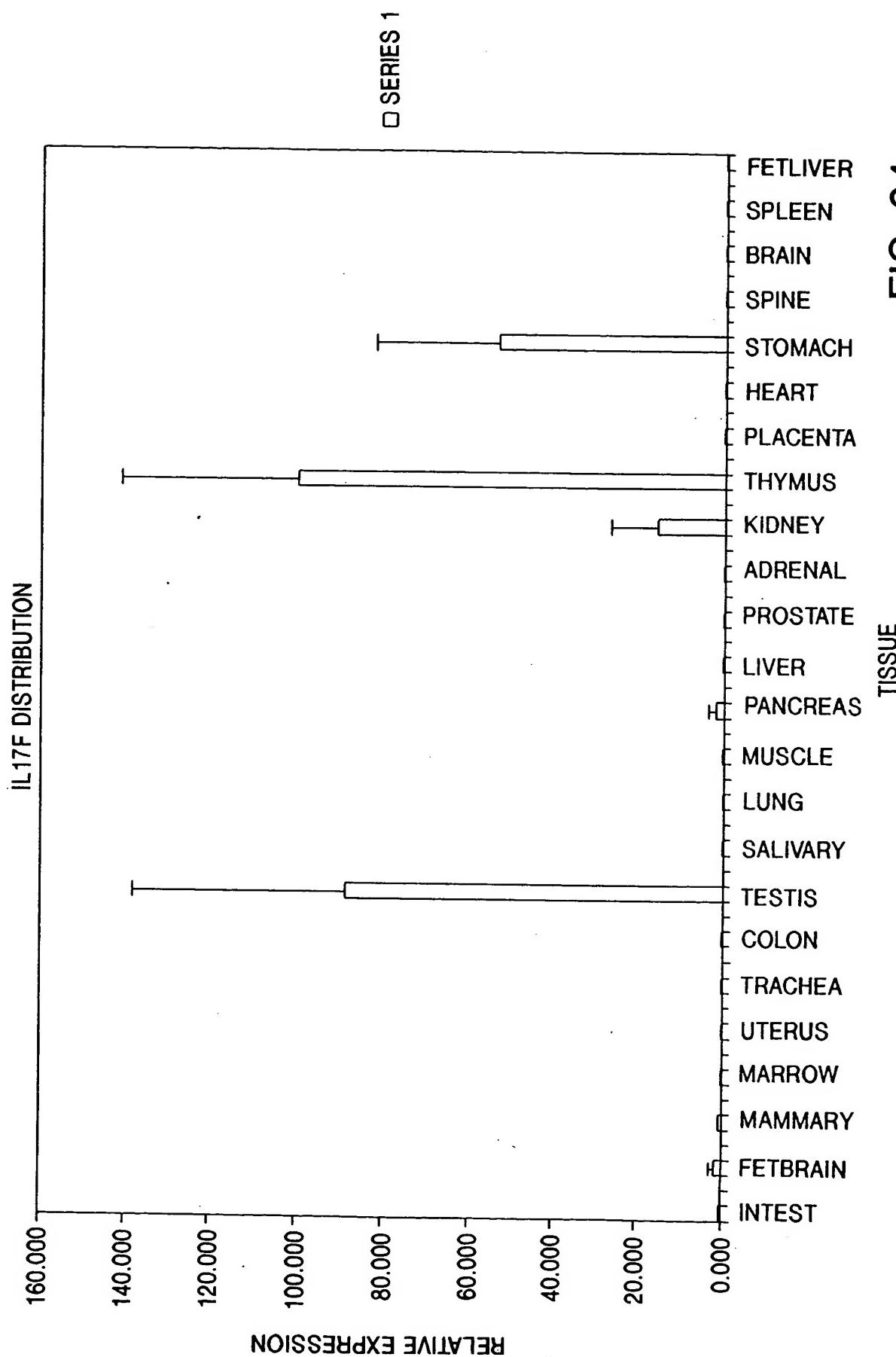


FIG. 25

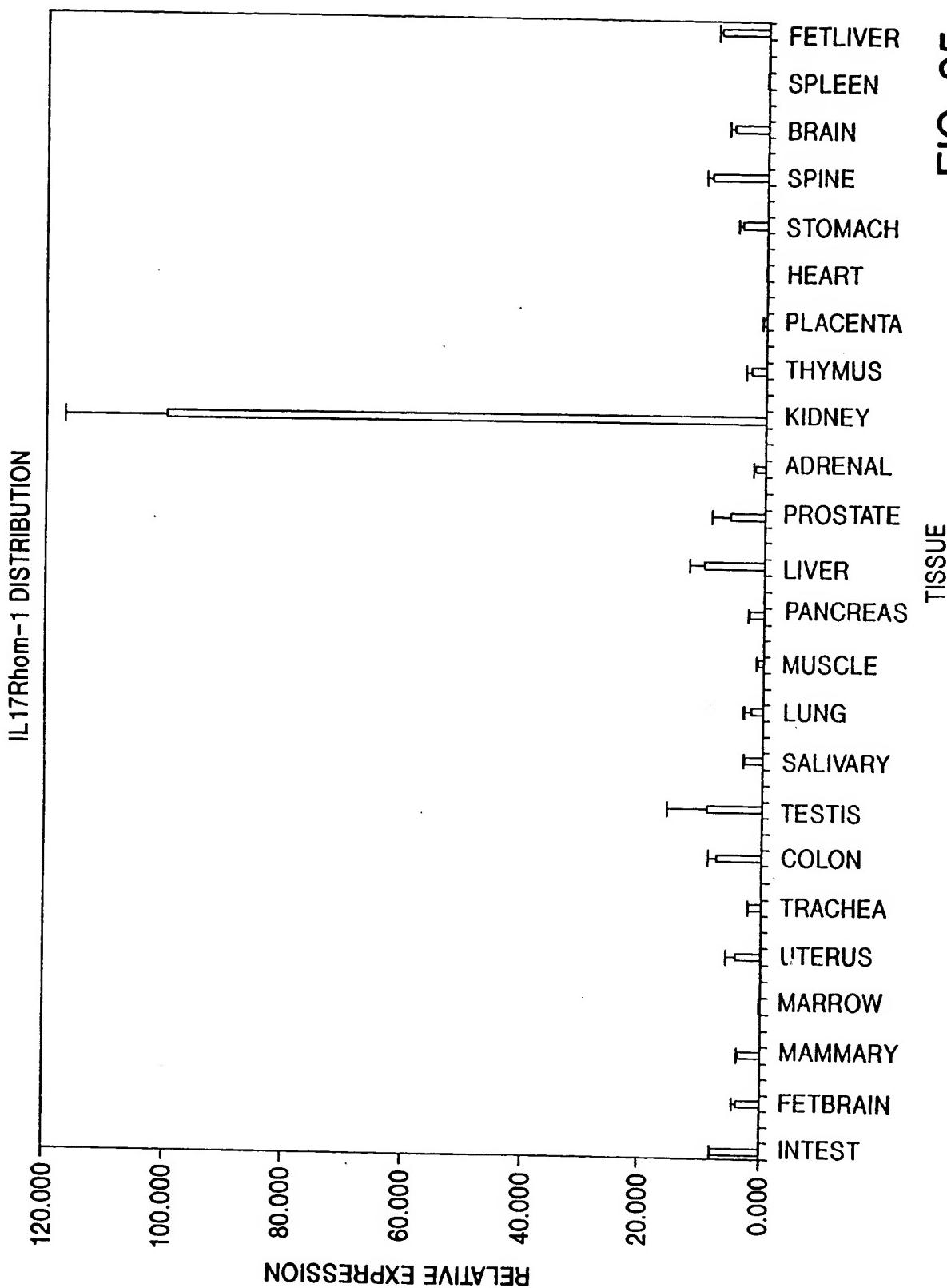


FIG. 26

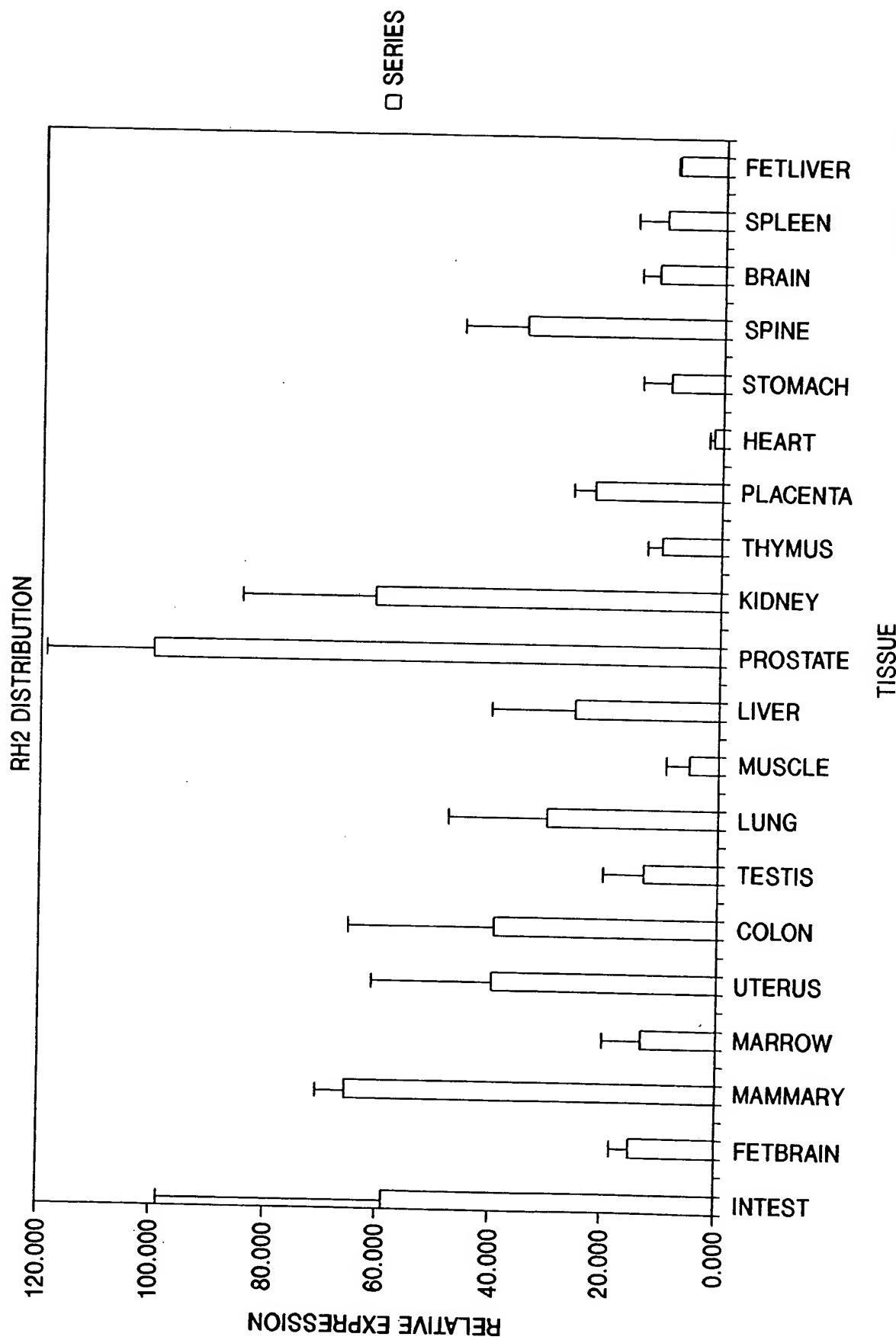


FIG. 27

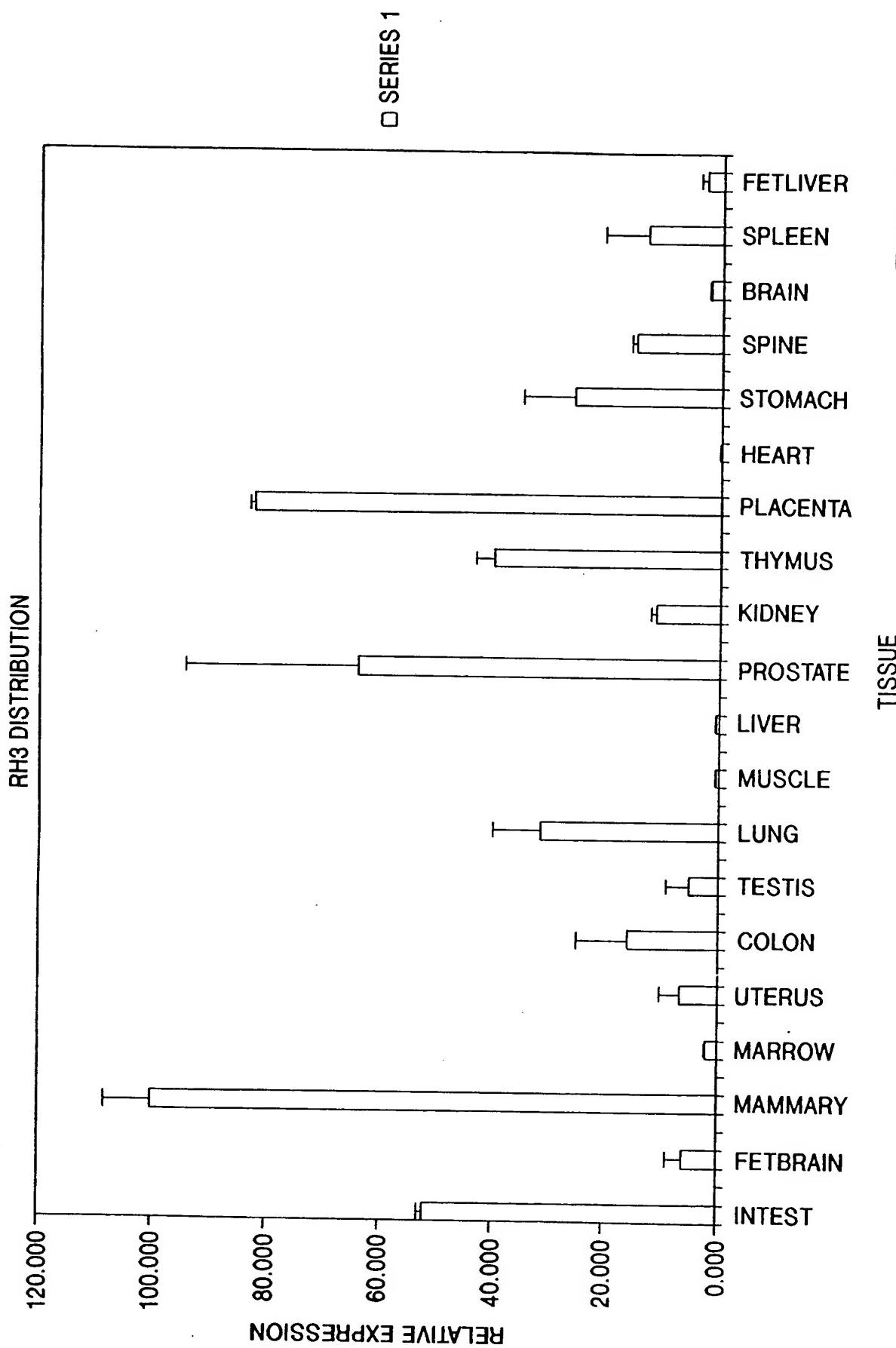
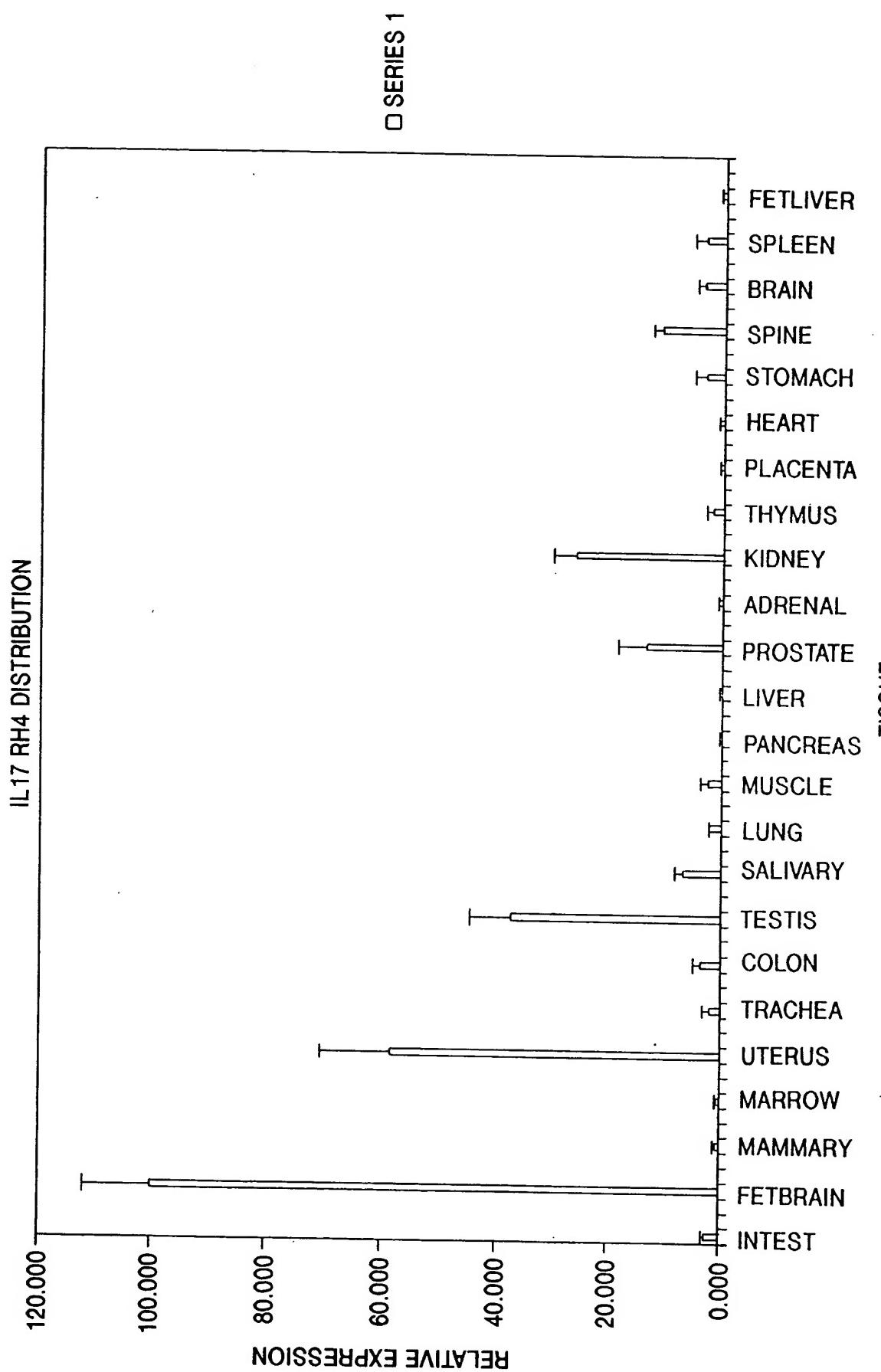


FIG. 28



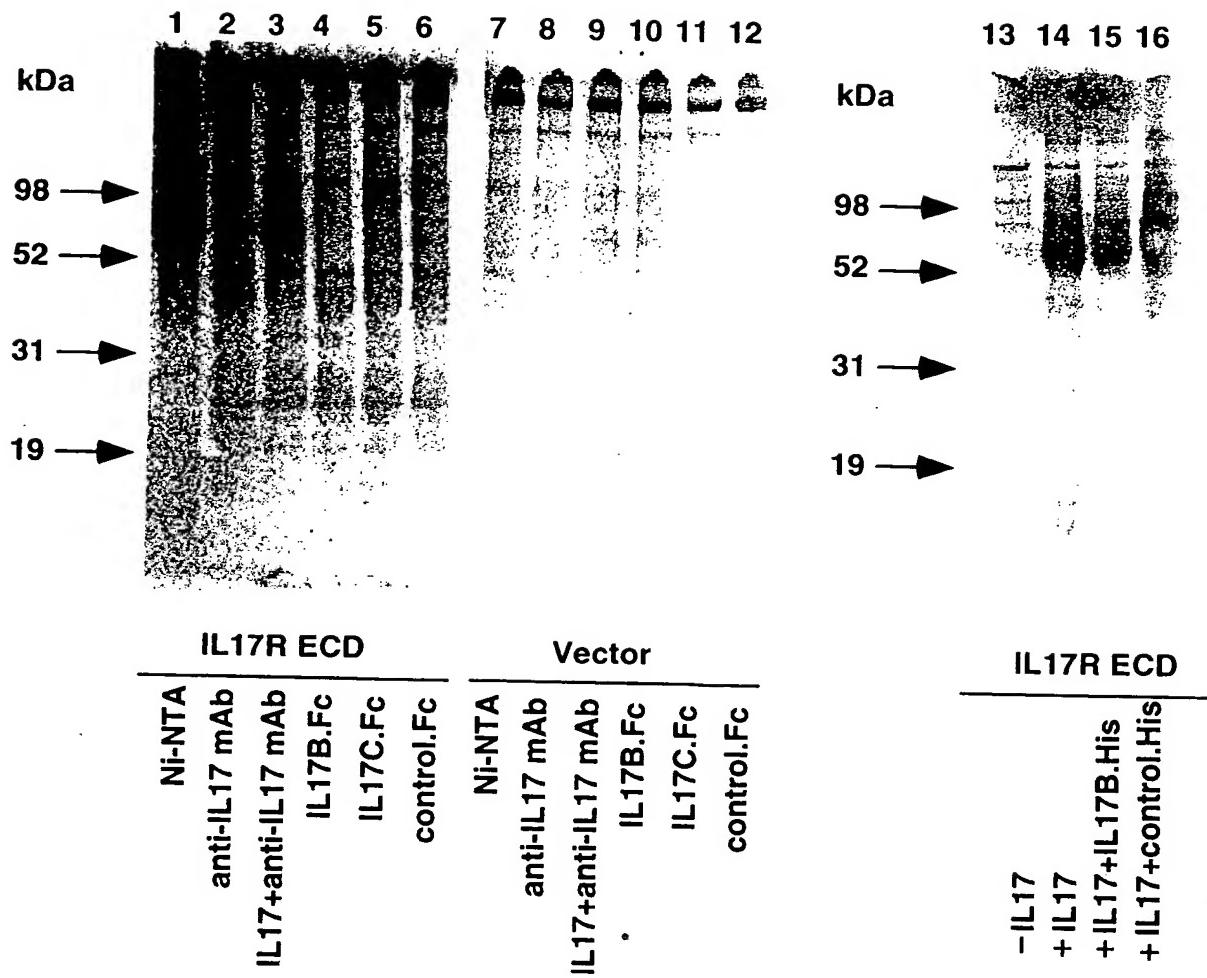


FIG. 29A

FIG. 29B

h-IL17 1 - - - - M T P G K T S L V S L L L S E A I V K A G I T I P R
 h-IL17B 1 - - - - M D W P H N L L F L L T I S I F L G L G Q P R S P K S K R K G Q G R P G P
 h-IL17C 1 - - - - M T L L P G L L F L L T W L H T C L A H H D P S L R G H P H S H G T P H C Y S A E E L P L G Q
 h-IL17E 1 M R E R P R L G E D S S L I S L F Q V V A F L A M V M G T H T Y S H W P S C C P

h-IL17 30 - - - - N P G C P N S E D K N F P R T V M V N L N I H N R N T N P K R
 h-IL17B 39 A P G P H Q V P L D L V S R M K P Y A R M E E Y E R N I E E M V A Q L R N S S E L A Q R K C E V N L
 h-IL17C 47 A P P H L L A R G A K W G Q A L P V A L V S S L E A A S H R G R H E R P S A T T T Q C P V L R P E E V
 h-IL17E 42 - - - - S K G Q D T S E E L L R W S T V P V P P L E P A R P N R H P E S C R A S E . . .

h-IL17 63 - S S D Y Y N R S T S P W N L H R N E D P E R Y P S V I W E A K C R H L G C I N A D G
 h-IL17B 89 Q L W M S N K R S L S P W G Y S I N H D P S R I P V D L P E A R C L C L G C V N P F T M Q E D R S M
 h-IL17C 97 L E A D T H Q R S I S P W Y R V D T D E D R Y P Q K L A F A E E C L C R G C I D A R T G
 h-IL17E 79 . D G P L N S R A I S P W R Y E L D R D L N R L P Q D L Y H A R C L C P H C V S L Q T G S H M D P R

h-IL17 110 M N S V P I Q Q E I L V L R E
 h-IL17B 139 V S V P V F S Q V P V R R R L C P P
 h-IL17C 146 L N S V R L L Q S L L V L R R P C S R D G S G L P T P G A F A E F H T E F H V P V G C T C V L P R
 h-IL17E 128 G N S E L L Y H N Q T V F Y R R P C H G E K
 h-IL17 151 V H H V A
 h-IL17C 196 S V
 h-IL17E 175 V M G . . .

FIG. 30

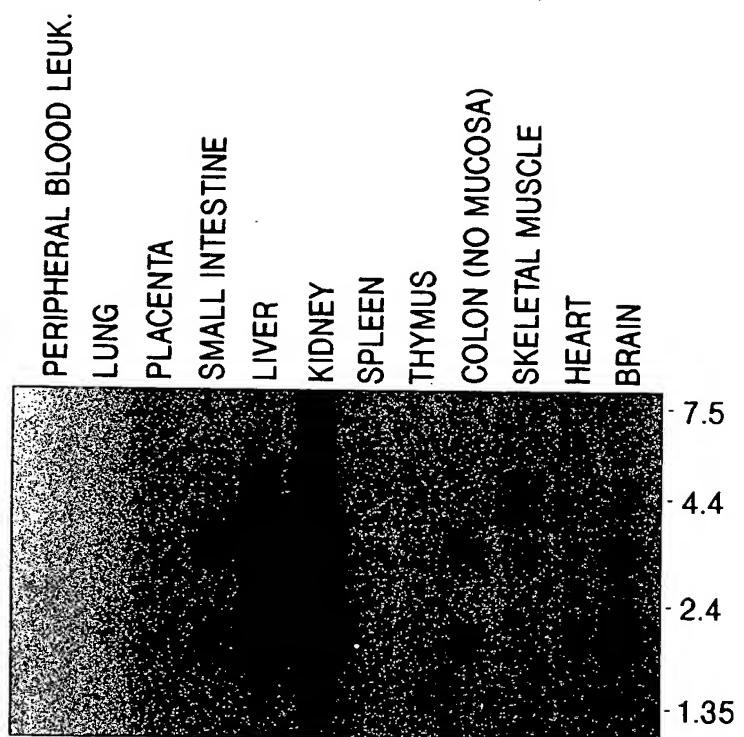


FIG. 31A

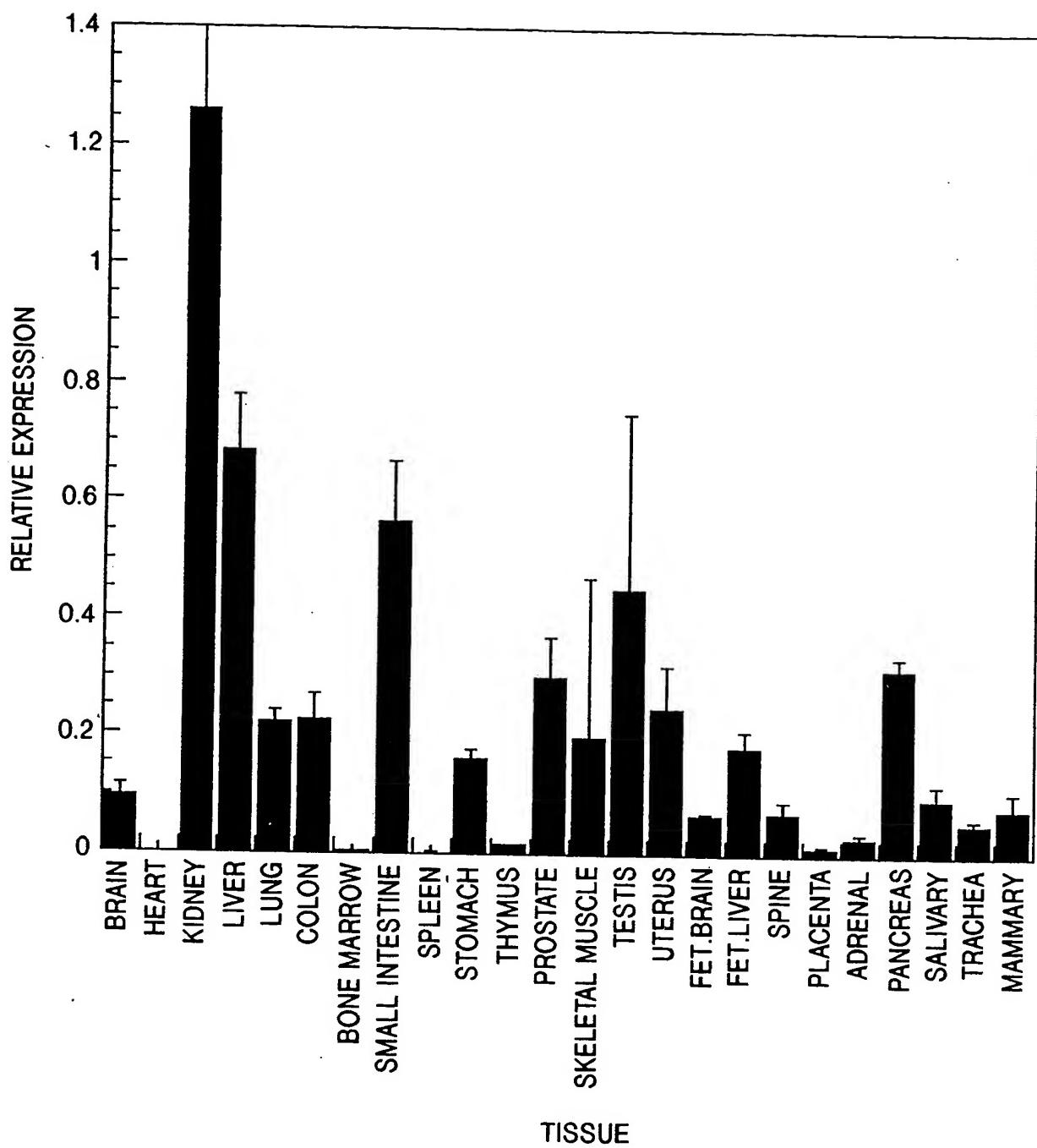


FIG. 31B

FLUORESCENCE INTENSITY

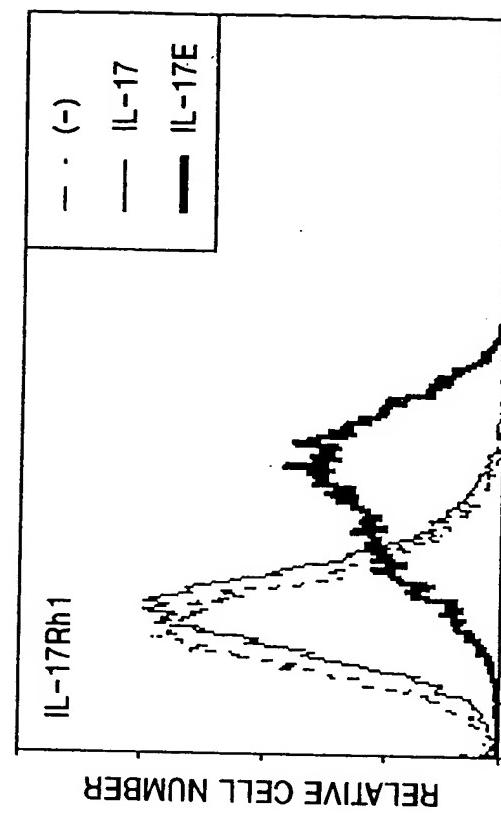
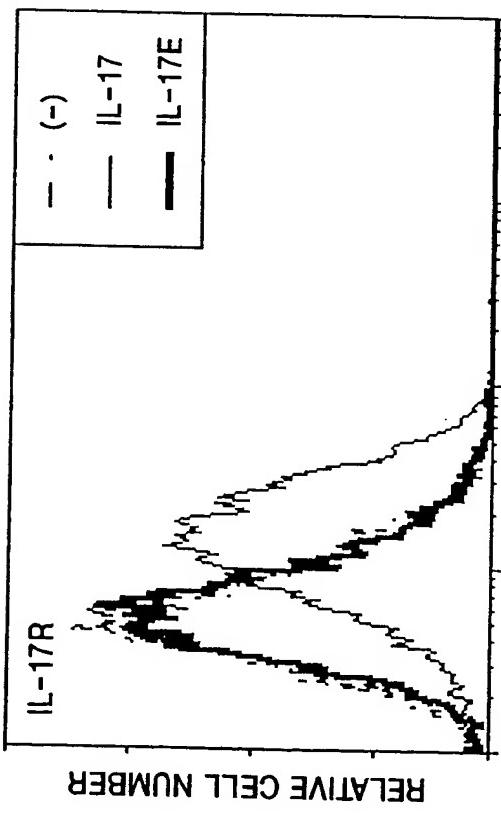


FIG. 32A

FLUORESCENCE INTENSITY



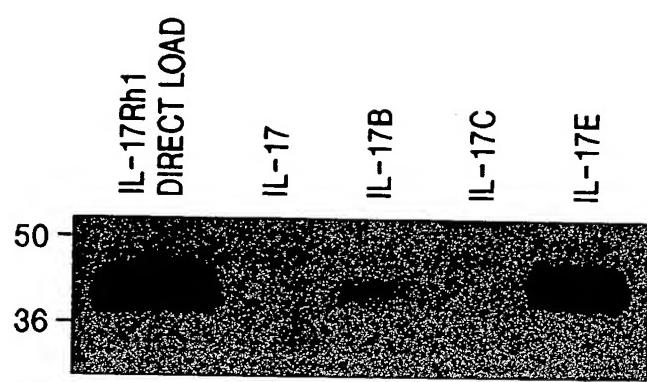


FIG. 32B

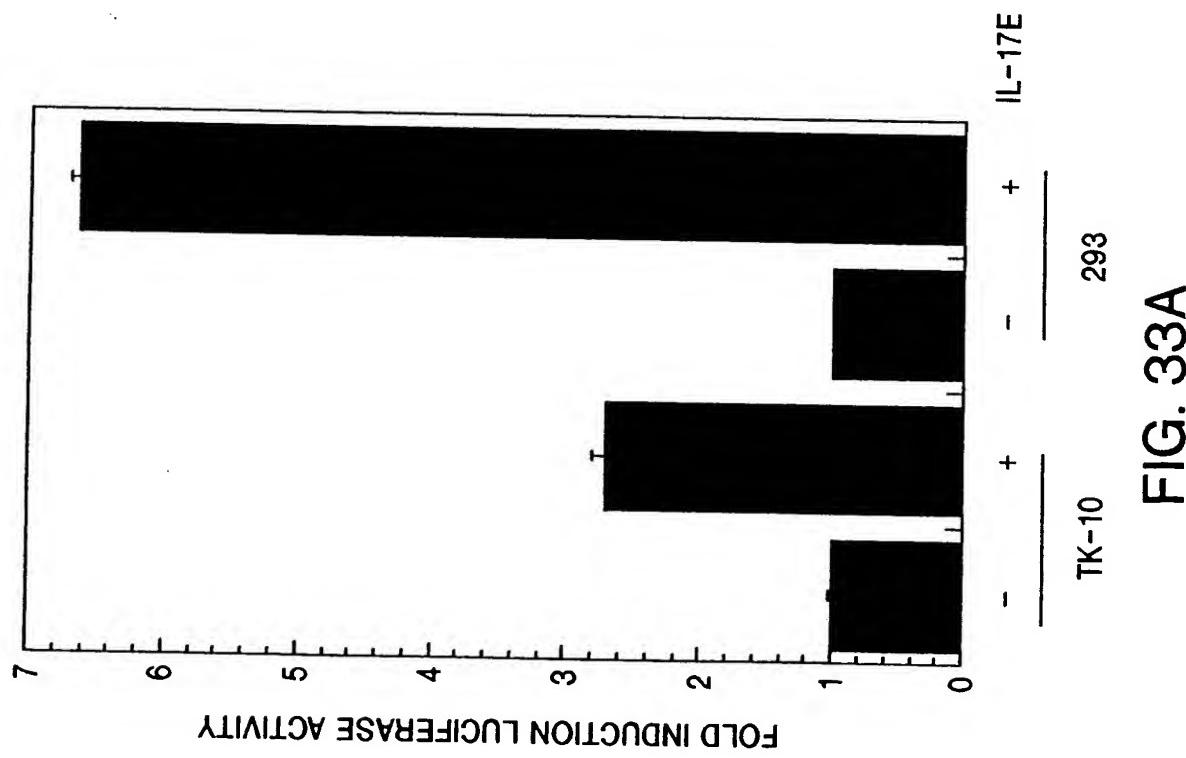
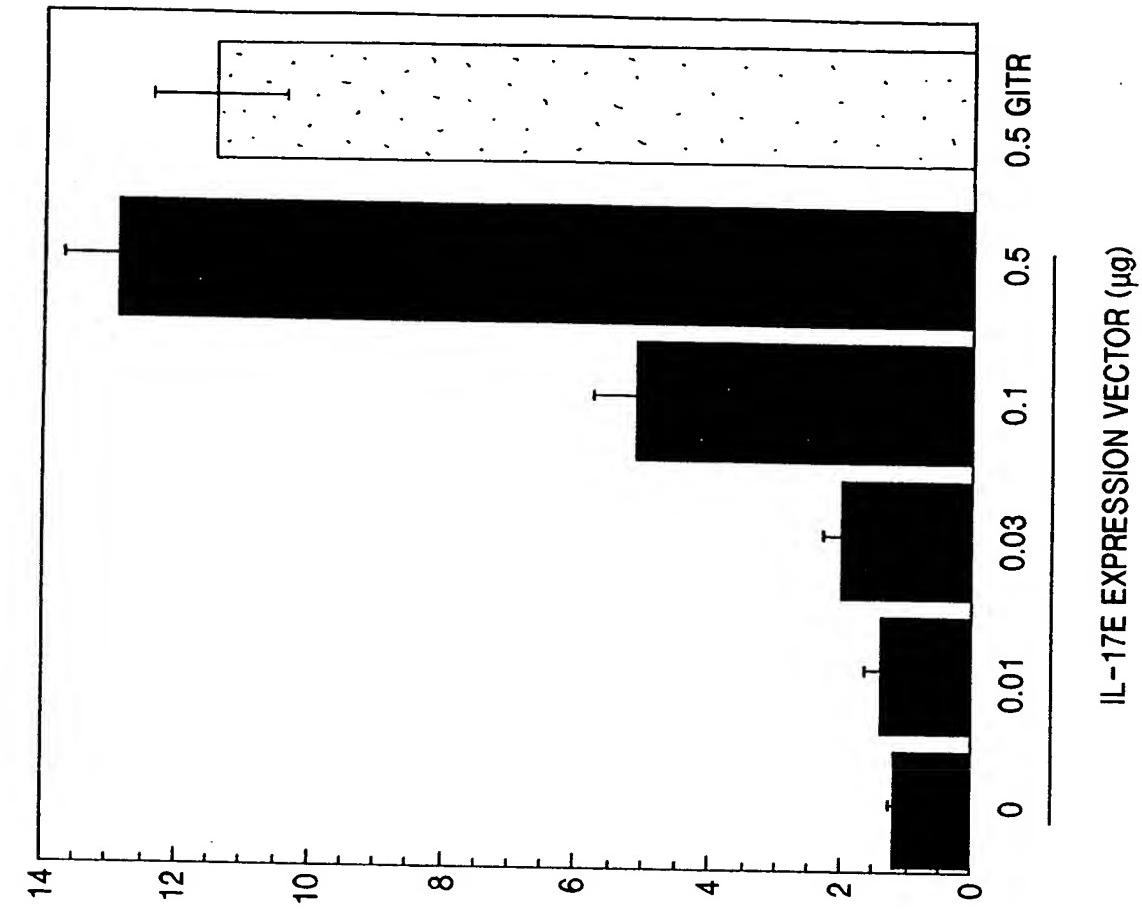


FIG. 33A



IL-17E EXPRESSION VECTOR (μg)

FIG. 33B

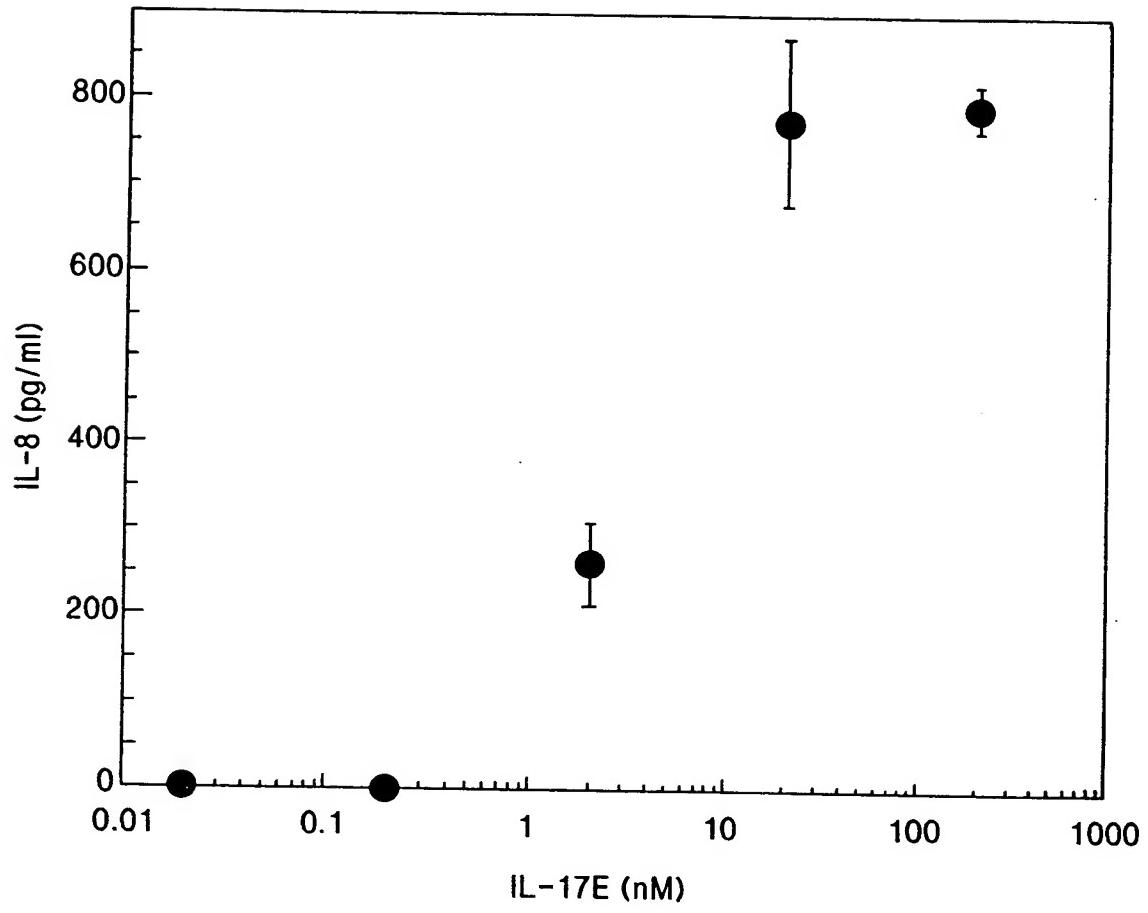


FIG. 34

IL-17 FAMILY OF CYTOKINES HAS COMPLEX PATTERN
OF OVERLAPPING RECEPTOR-LIGAND SPECIFICITIES

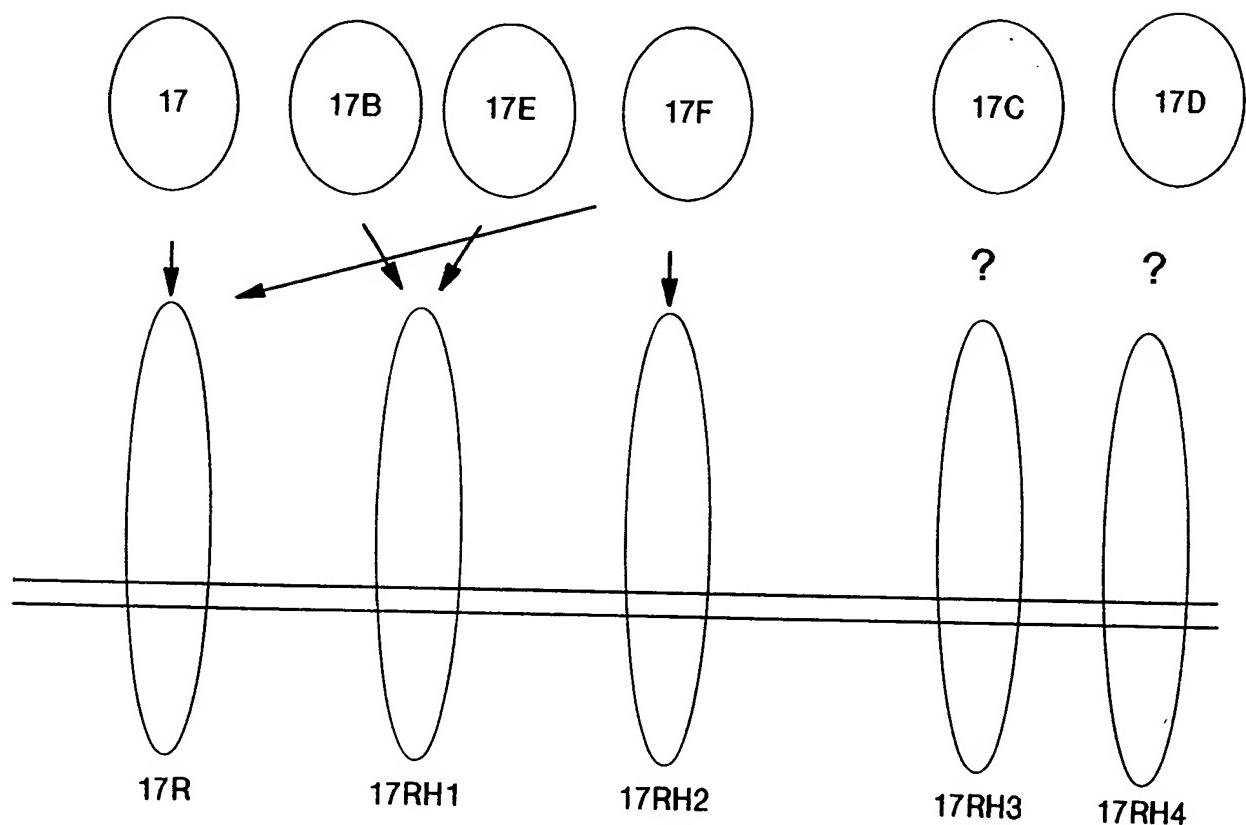


FIG. 35

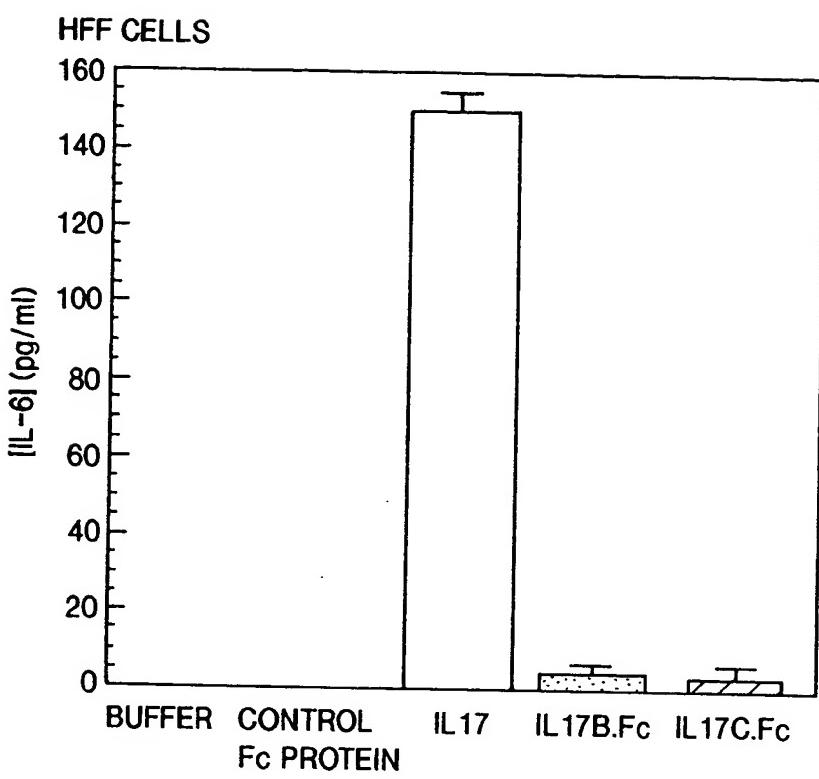


FIG. 36A

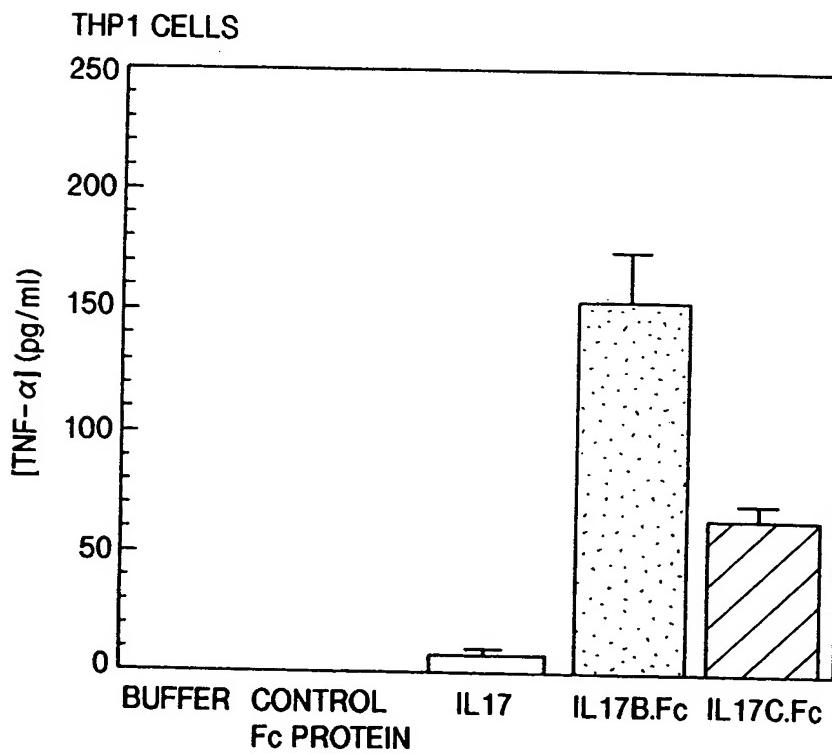
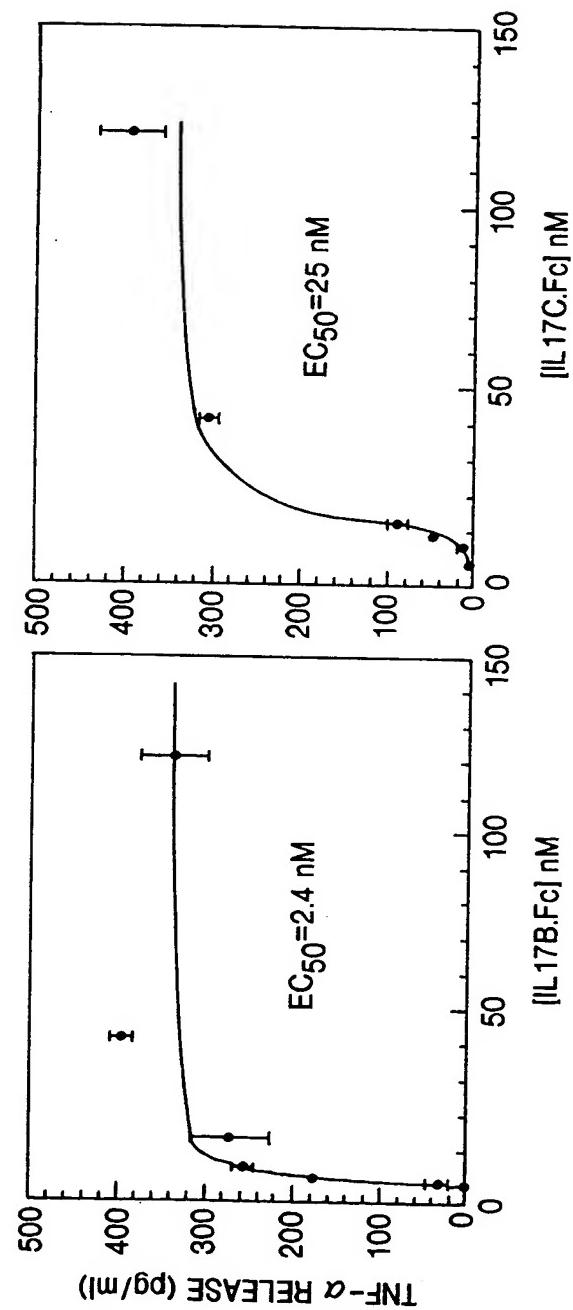
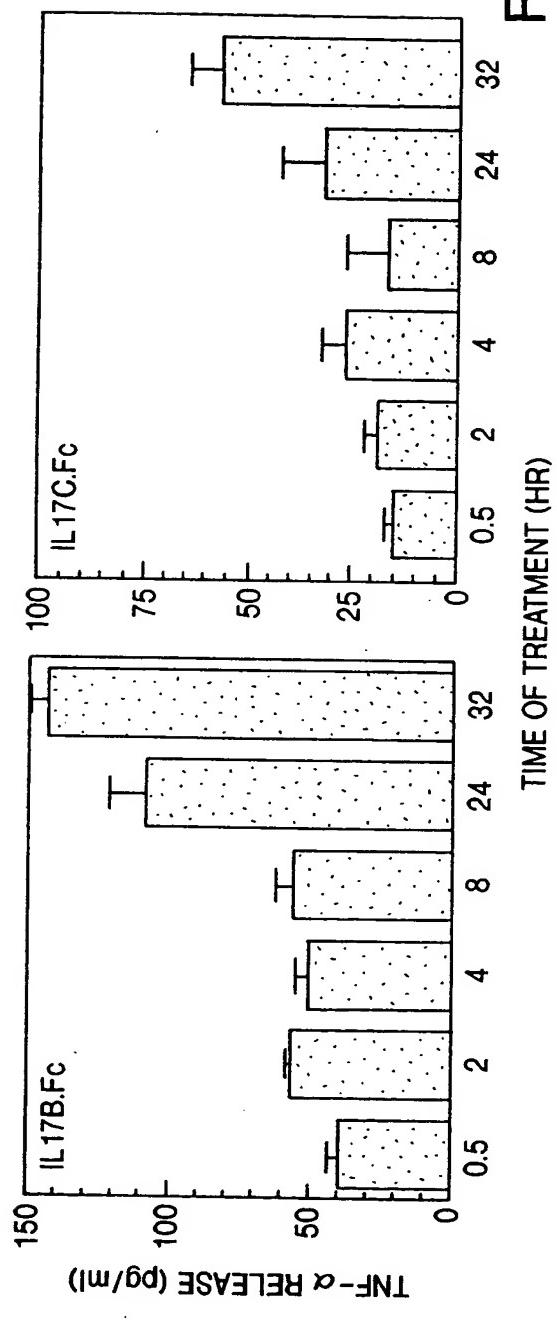


FIG. 36B



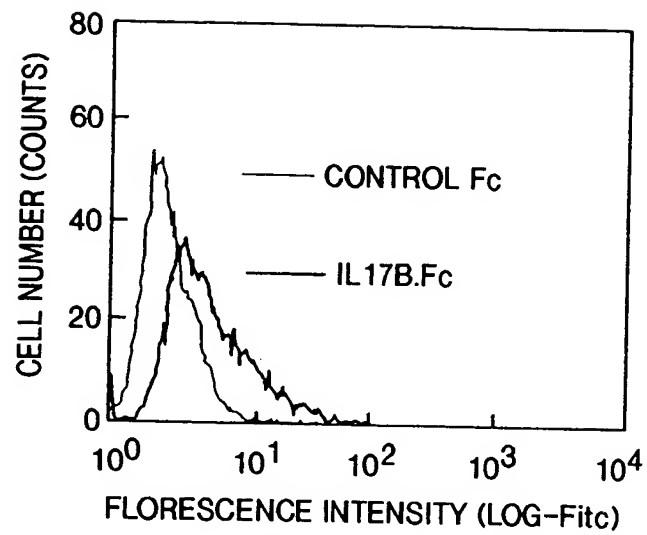


FIG. 38A

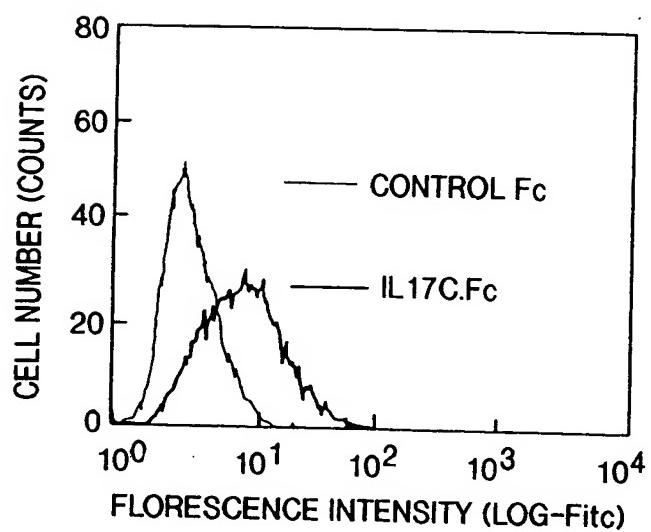


FIG. 38B

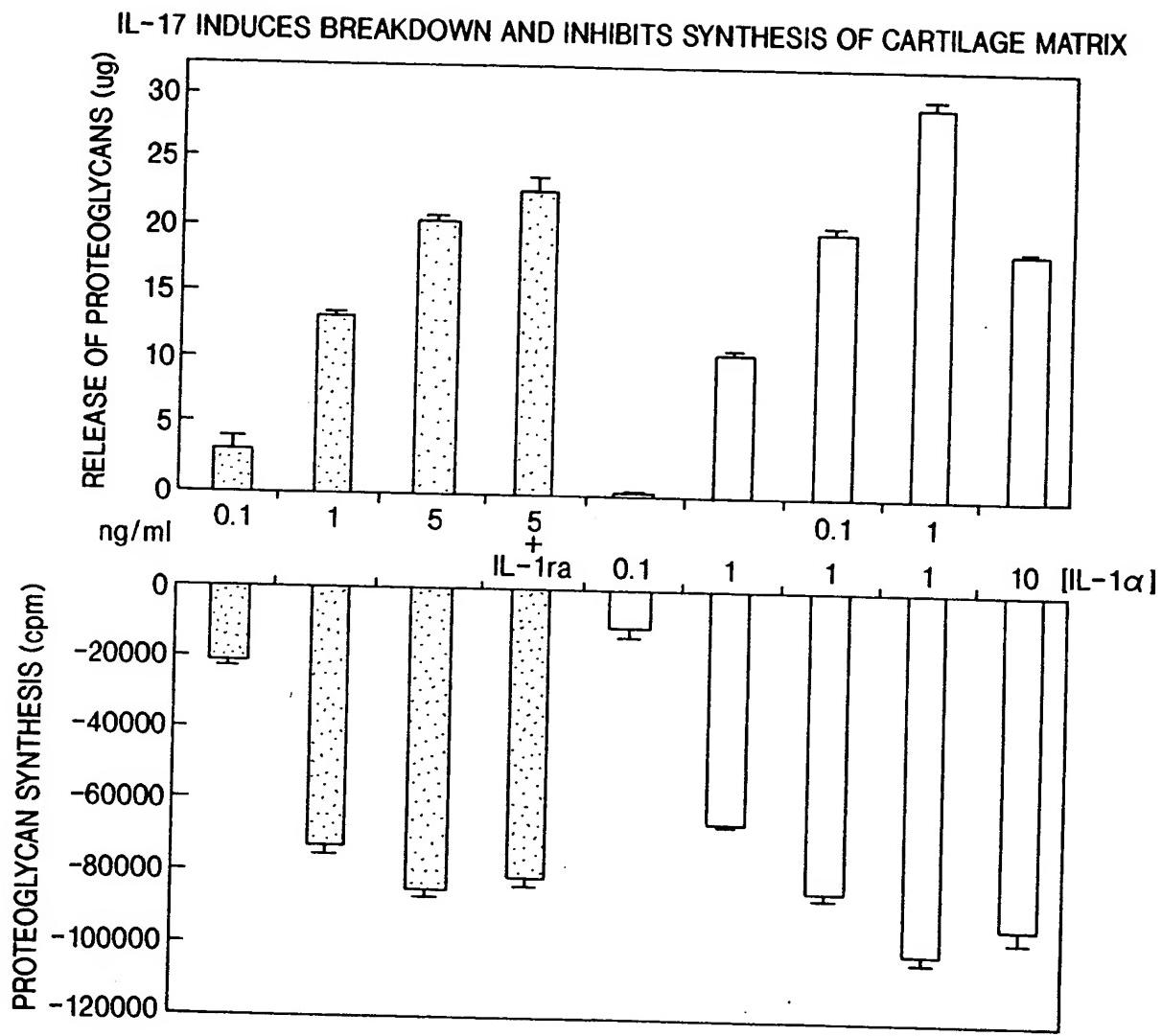


FIG. 39

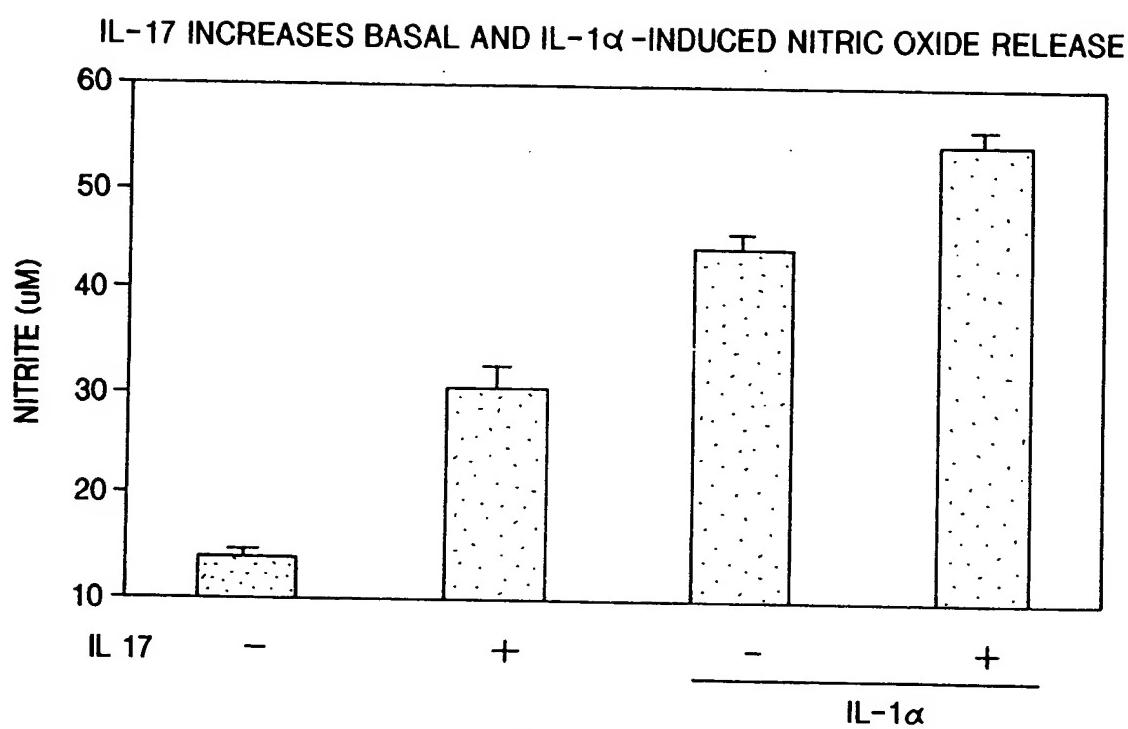


FIG. 40

INHIBITION OF NITRIC OXIDE RELEASE DOES NOT BLOCK THE DETRIMENTAL EFFECTS OF IL 17 ON MATRIX BREAKDOWN OR SYNTHESIS

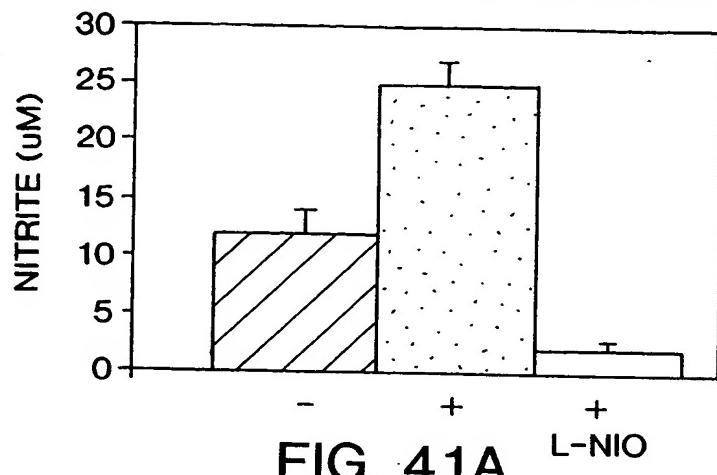


FIG. 41A

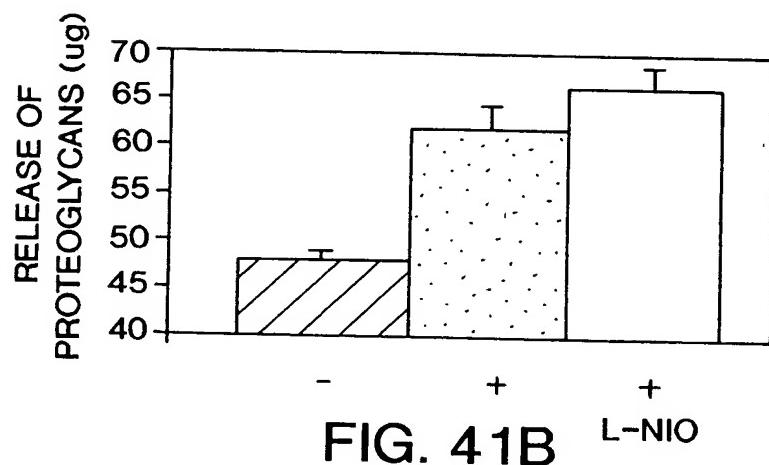


FIG. 41B

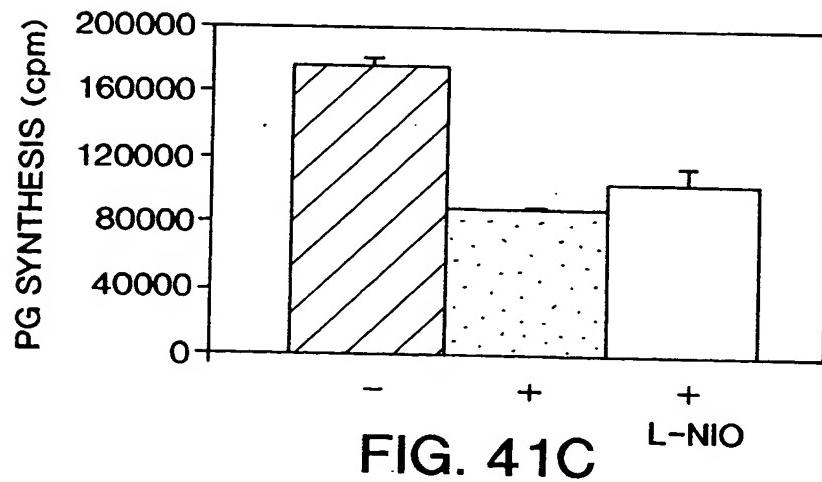


FIG. 41C

**INHIBITION OF NO RELEASE ENHANCES IL1- α -INDUCED
MATRIX BREAKDOWN BUT NOT MATRIX SYNTHESIS**

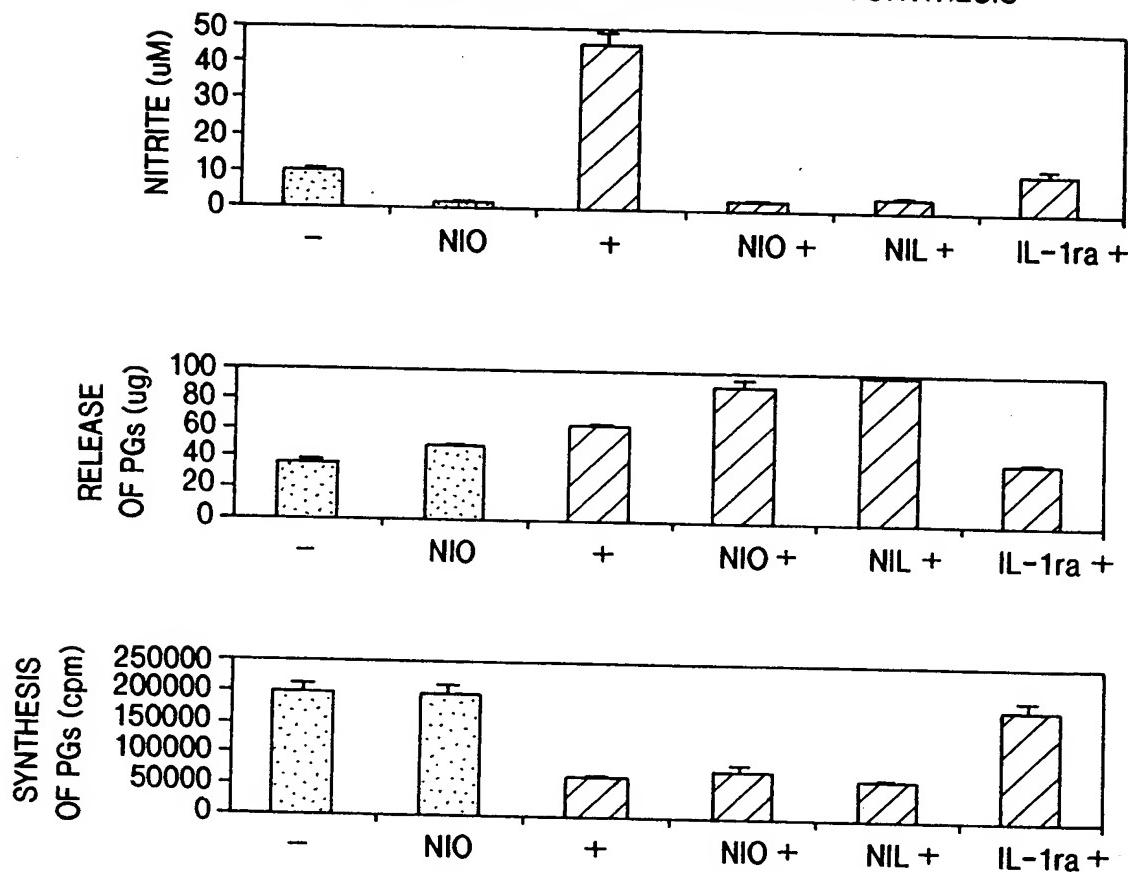


FIG. 42

IL-17C DETRIMENTAL EFFECTS ON ARTICULAR CARTILAGE

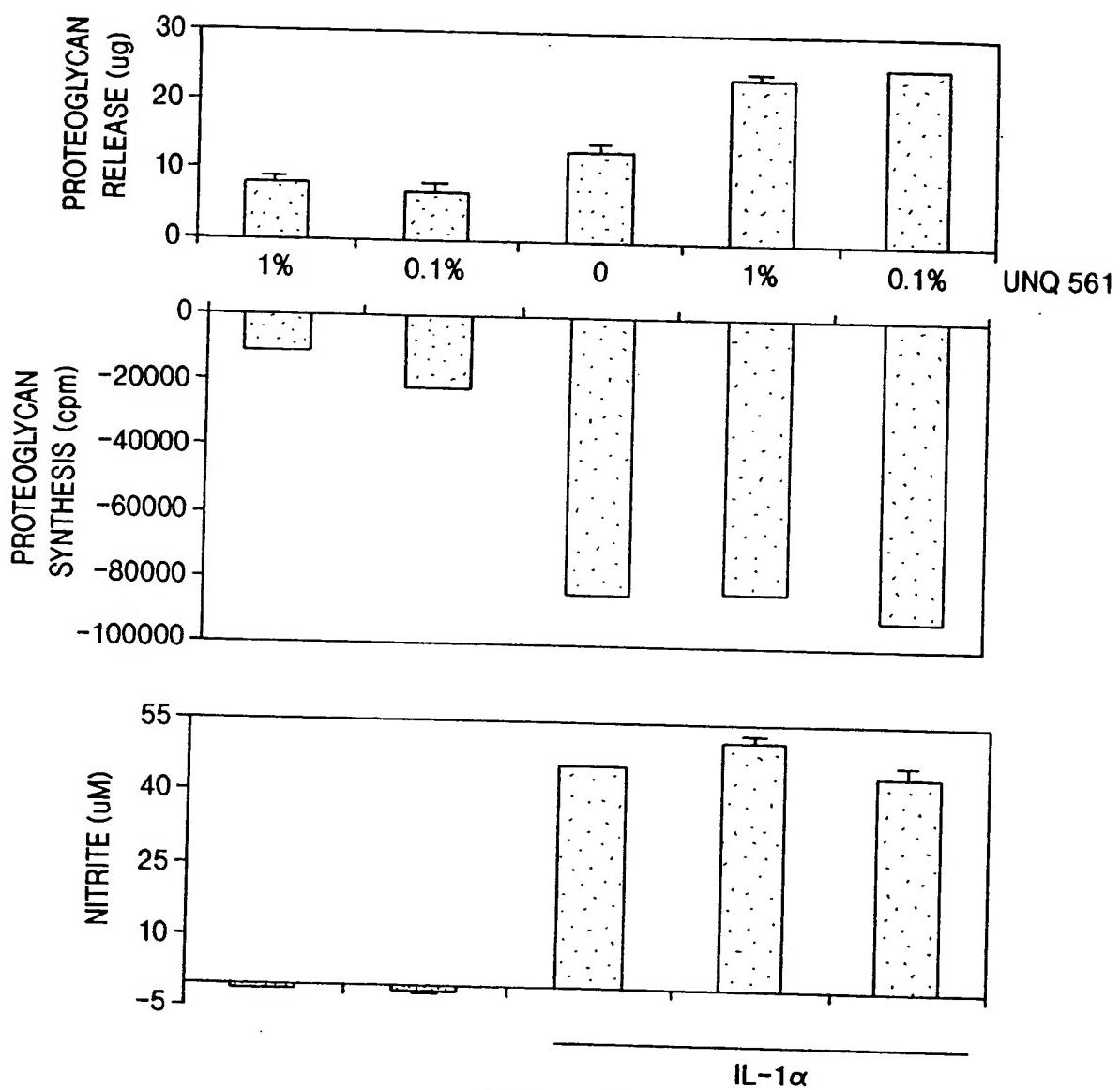


FIG. 43

INFLAMMATORY BOWEL DISEASE:
EXPRESSION OF IL-17 FAMILY IN MOUSE MODEL OF IBD

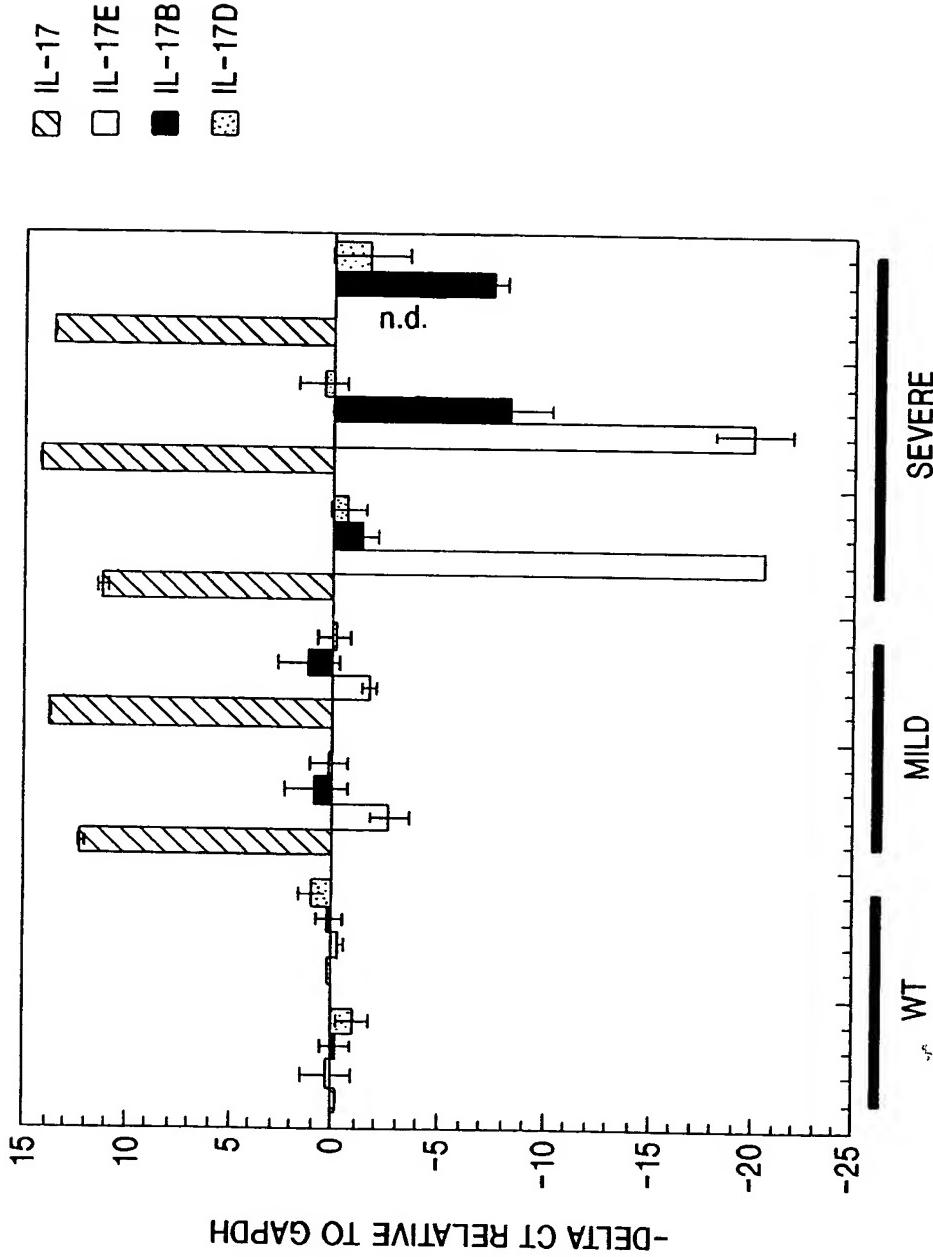


FIG. 44

IL-17D, PRESENT IN BRAIN, DECREASES RAPIDLY FOLLOWING STROKE

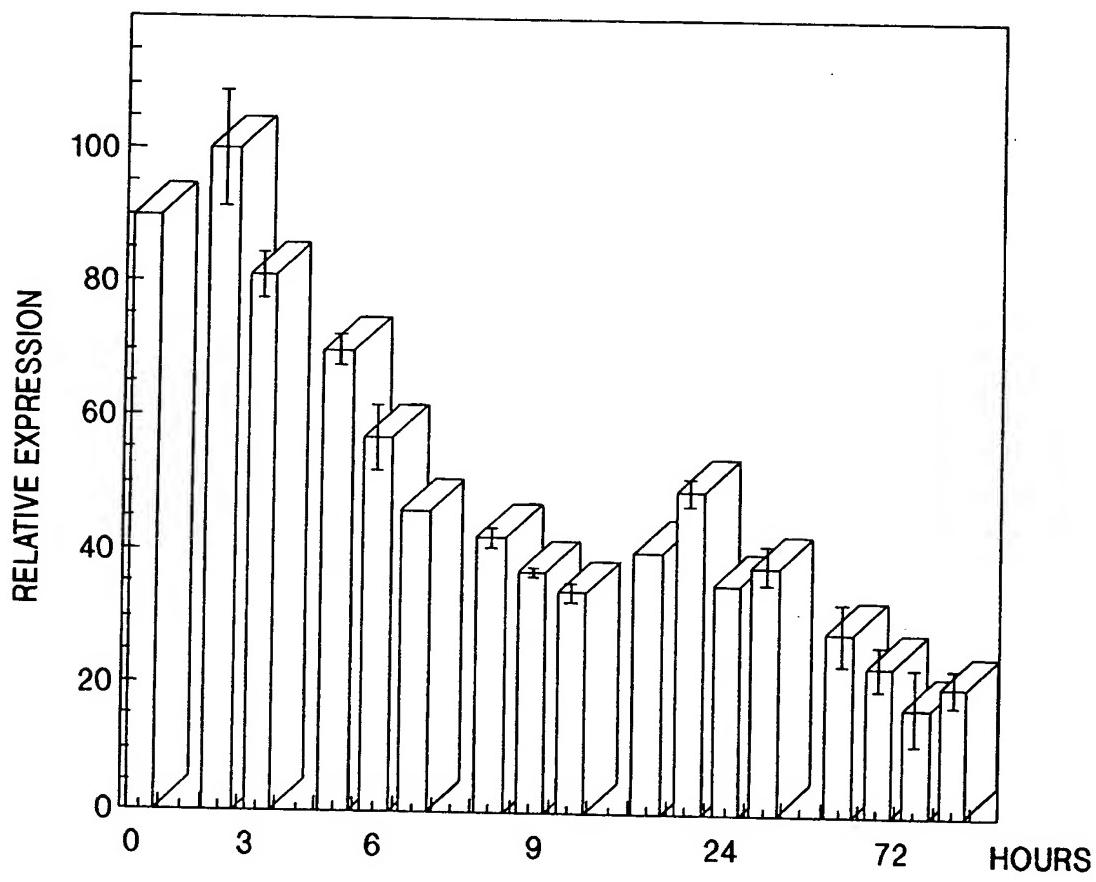


FIG. 45

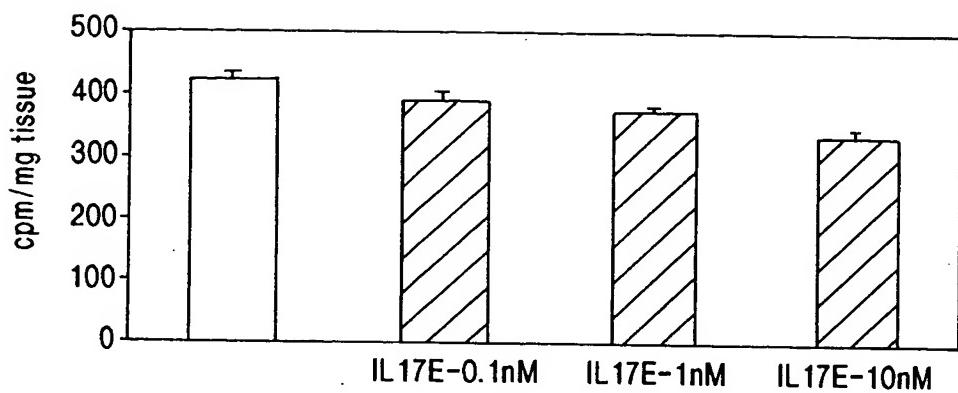


FIG. 46A

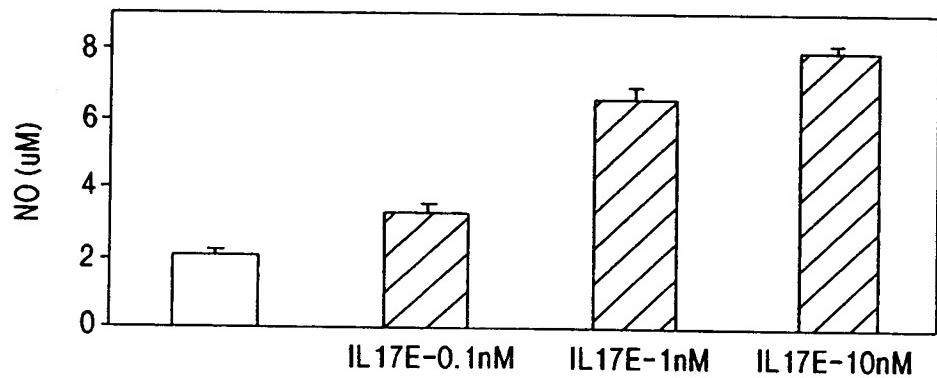


FIG. 46B

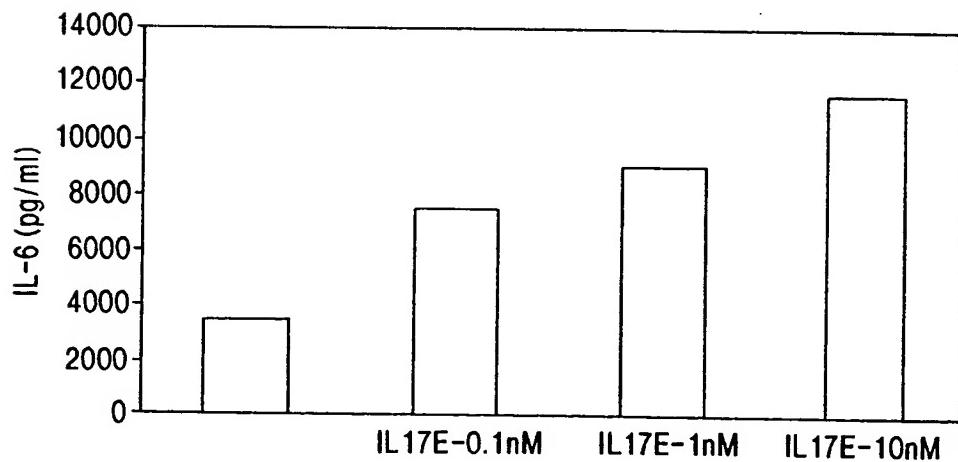


FIG. 46C

FIG. 47A

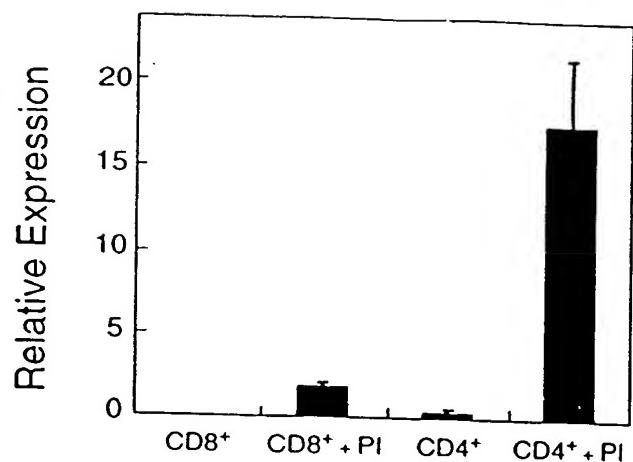


FIG. 47B

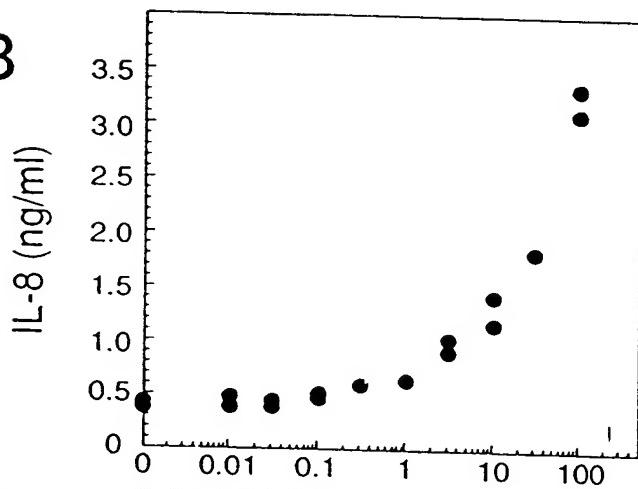
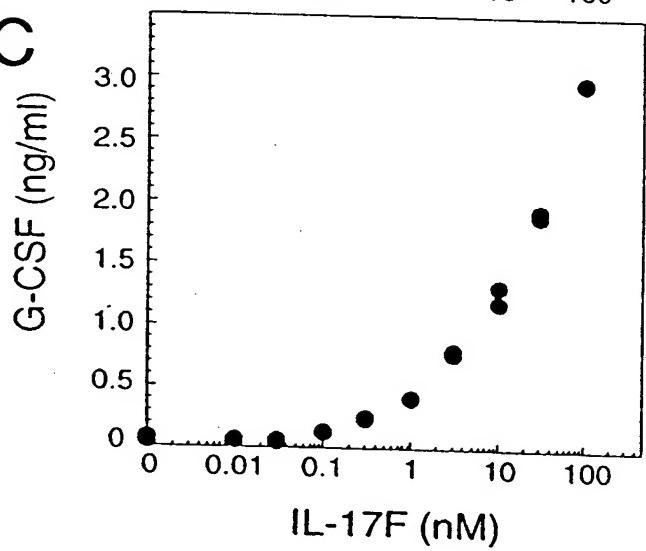


FIG. 47C



Matrix Breakdown

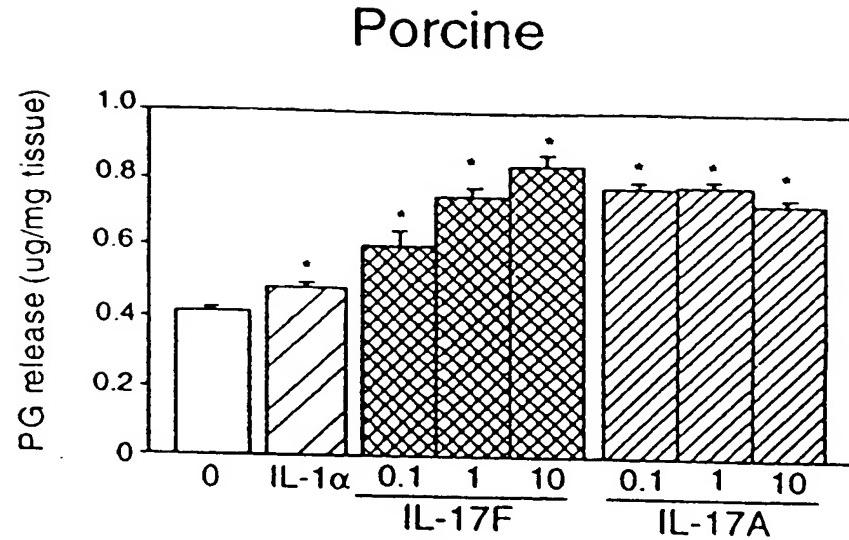


FIG. 48A

Matrix Synthesis

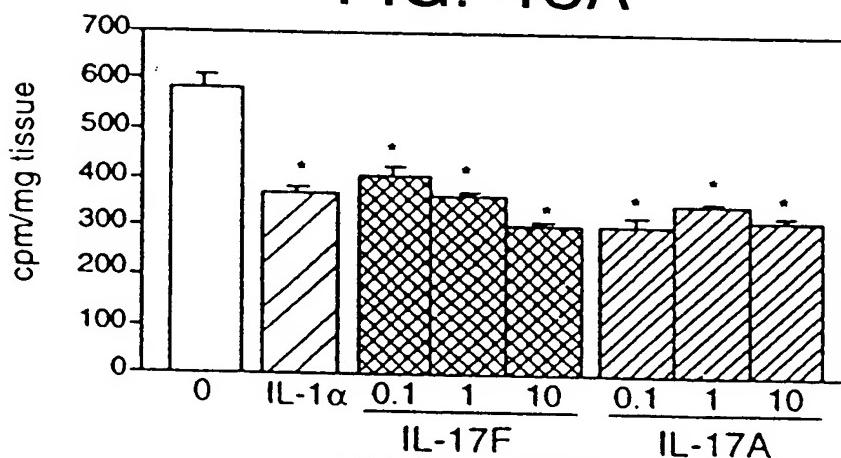


FIG. 48B

IL-6 production

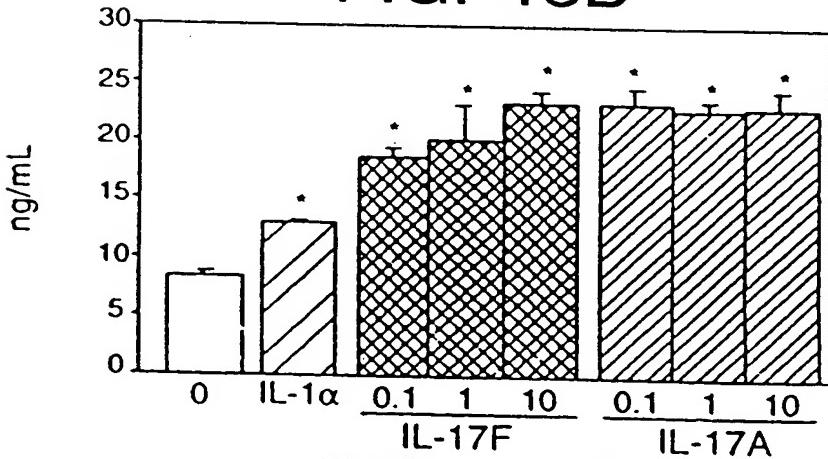


FIG. 48C

**Matrix
Breakdown**

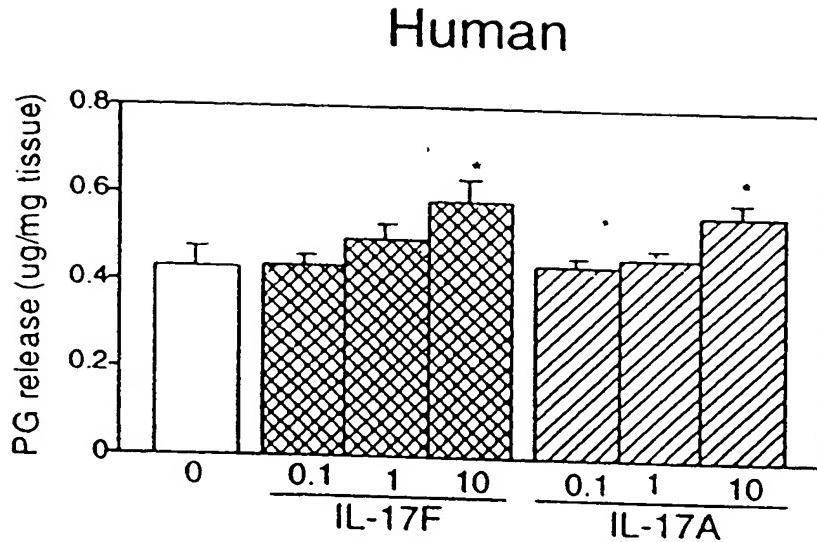


FIG. 48D

**Matrix
Synthesis**

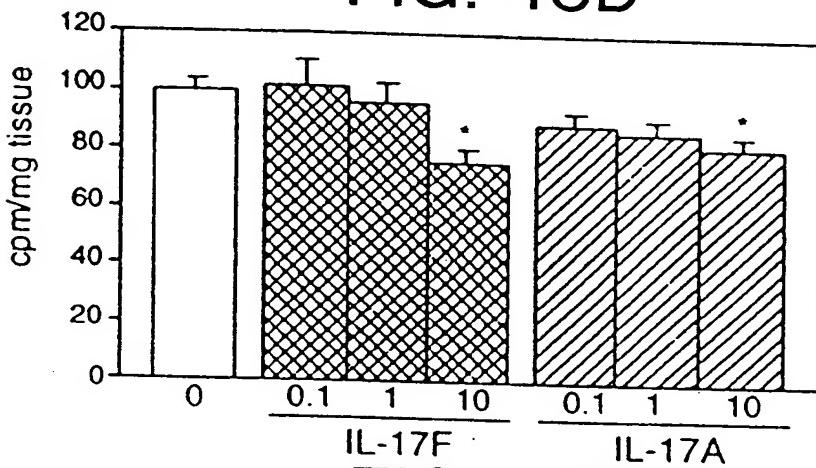


FIG. 48E

**IL-6
production**

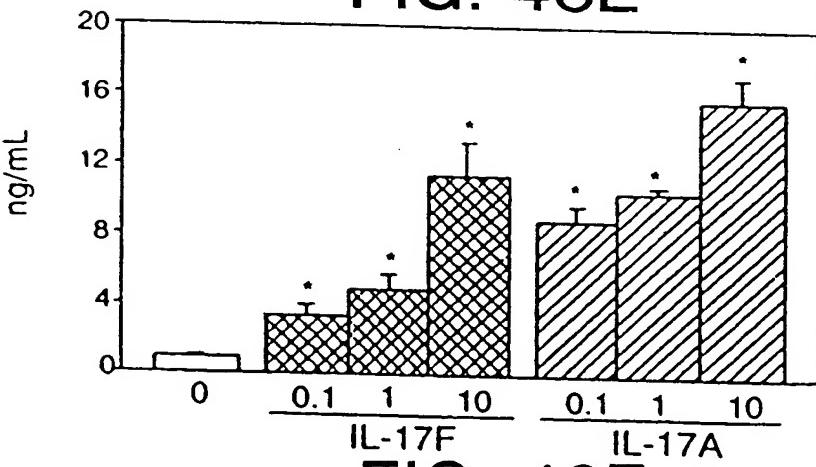


FIG. 48F

FIG. 49C

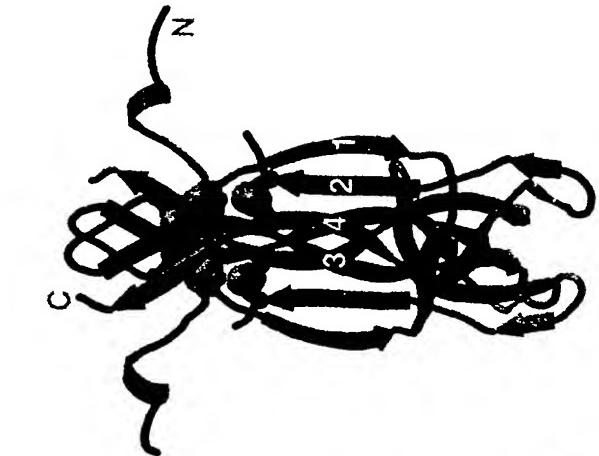


FIG. 49B

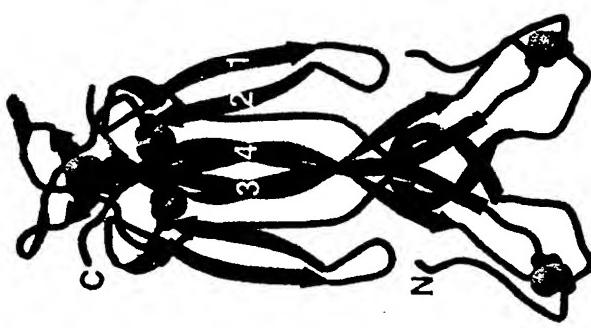
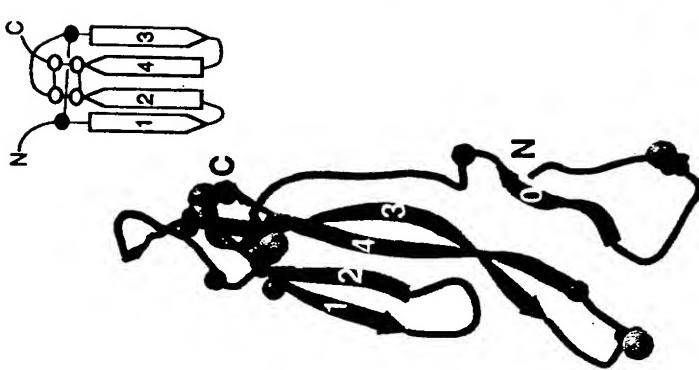


FIG. 49A



*

IL-17F	RKIPKVG	HFFFQKPE	17
IL-17A	IVKAG	ITIPRNE.G.	14
IL-17BQPRS	PKSKRKQGQR	PGPLAPGPHQ	VPLDLVSRMK	PYARMEEYER	44
IL-17C	HHDPSLRGHP	HSHGTPHYS	AEELPLGQAP	PHLLARGAKW	GQALPVALVS	50
IL-17EYS	HWPS.GPSKG	QDTSEELLRW	22

IL-17F	PPVPGG....	SMKLDI	GIINENQRVS	MSRNIESRST	PMNYTVTW	59
IL-17A	PNSEDKNFPR	TVMVNLIHN	RNTNTN..PK	RSDYYNRST	PWNLHRNED	62
IL-17B	NIEEMVAQLR	NSSELAQR	KCEV....NL	QLWMSNKRSI	PWGY SINHD	88
IL-17C	SLEASHRGR	HERPSATT	Q.PVLRPEEV	LEADTHQRSI	PWRYRVDTD	98
IL-17E	STVPVPPLEP	ARP NRHPE	S.RASE....	DGPLNSRAI	PWRYELDRD	65

IL-17F	PNRYPSEVVQ	AQ.RNLG.TN	A..QGKEDIS	MN.VPI.QQE	TLVVRKHQG	106
IL-17A	PERYP SVIWE	AK.RHLG.TN	A..DGNVDYH	MN.VPI.QQE	ILVLIRREPPH	109
IL-17B	PSRI PVDLPE	AR.LCIG.VN	PF.TMQEDRS	MV.VPV.FSQ	VPVRRR...L	133
IL-17C	EDRYPQKLA F	AE.LRG.ID	AR.TGRE TAA	LN.VRL.LQS	LLVLRR..RP	144
IL-17E	LNRLPQDLYH	AR.LCPH.VS	LQTGSHMDPR	GN.ELLYHNQ	TVFYRRP...	112

*						
IL-17F	SV.....	SPQLEK	VLI..VTVGCT	CATPVIIHHQ	...	133
IL-17A	CPN.....	SPRLEK	IL..MSVGCT	CATPIVRRVA	...	136
IL-17B	CPPPPRTGP.	CRQRA	VMETIAVGCT	C.I.F.....	...	160
IL-17C	CSRDGSGLPT	PGAFAFHTEF	IH..VPVGCT	CV.LPRSVAA	ALE	184
IL-17E	CHGEKGTHKGYLER	RLYRVSLACV	CYPRVMG...	...	145

FIG. 50

FIG. 51C

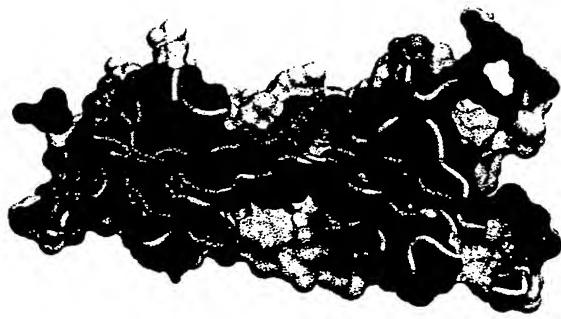


FIG. 51B

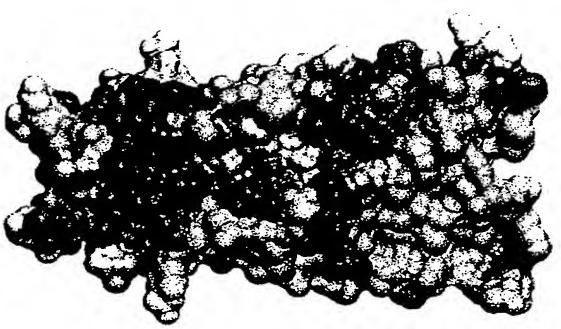


FIG. 51A

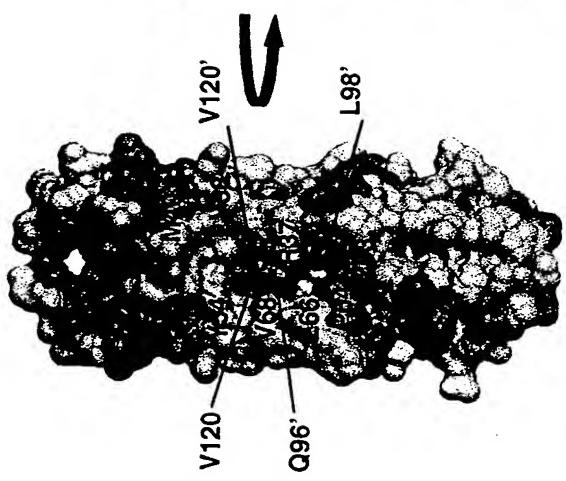


FIG. 52C

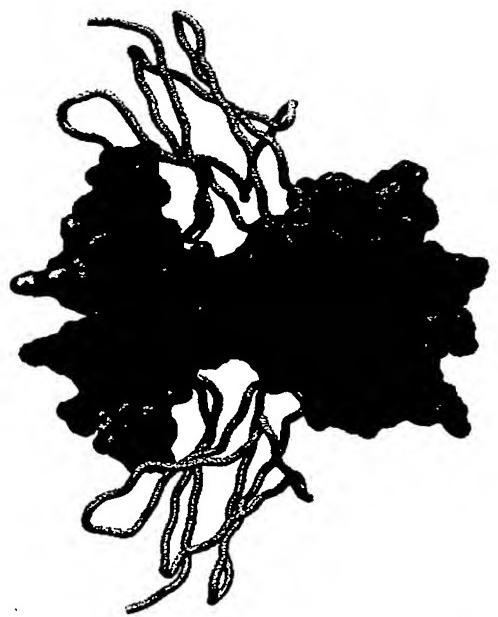


FIG. 52B

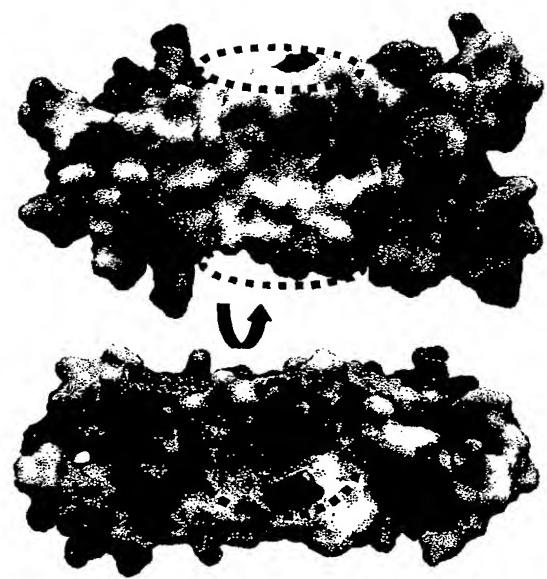
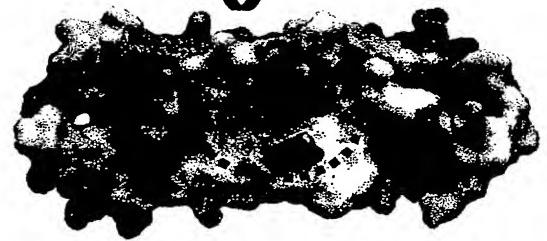


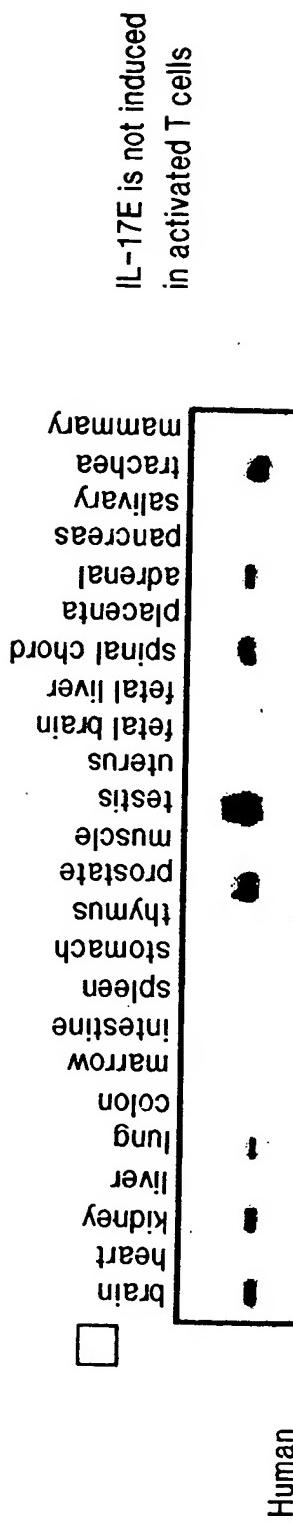
FIG. 52A



IL-17E is highly conserved between human and mouse

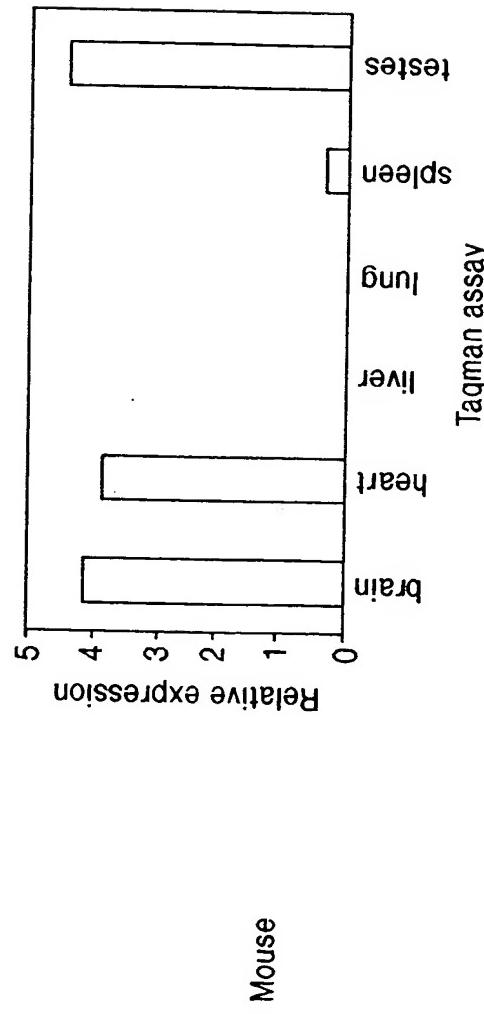
FIG. 53

Tissue distribution of IL-17E



IL-17E (PCR then probed with cDNA)

FIG. 54B



Taqman assay

FIG. 54A

mll-17E transgenics are growth retarded

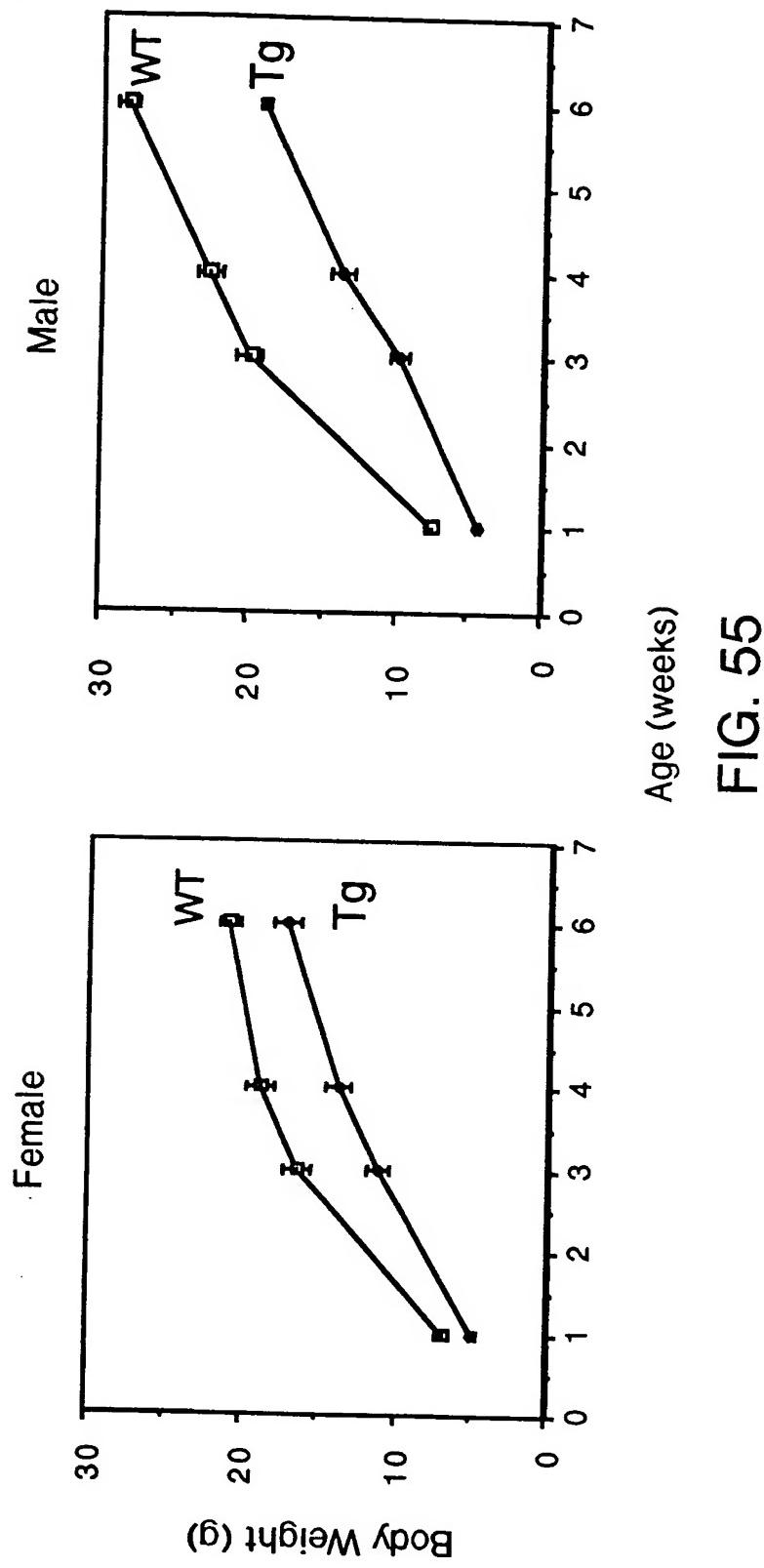
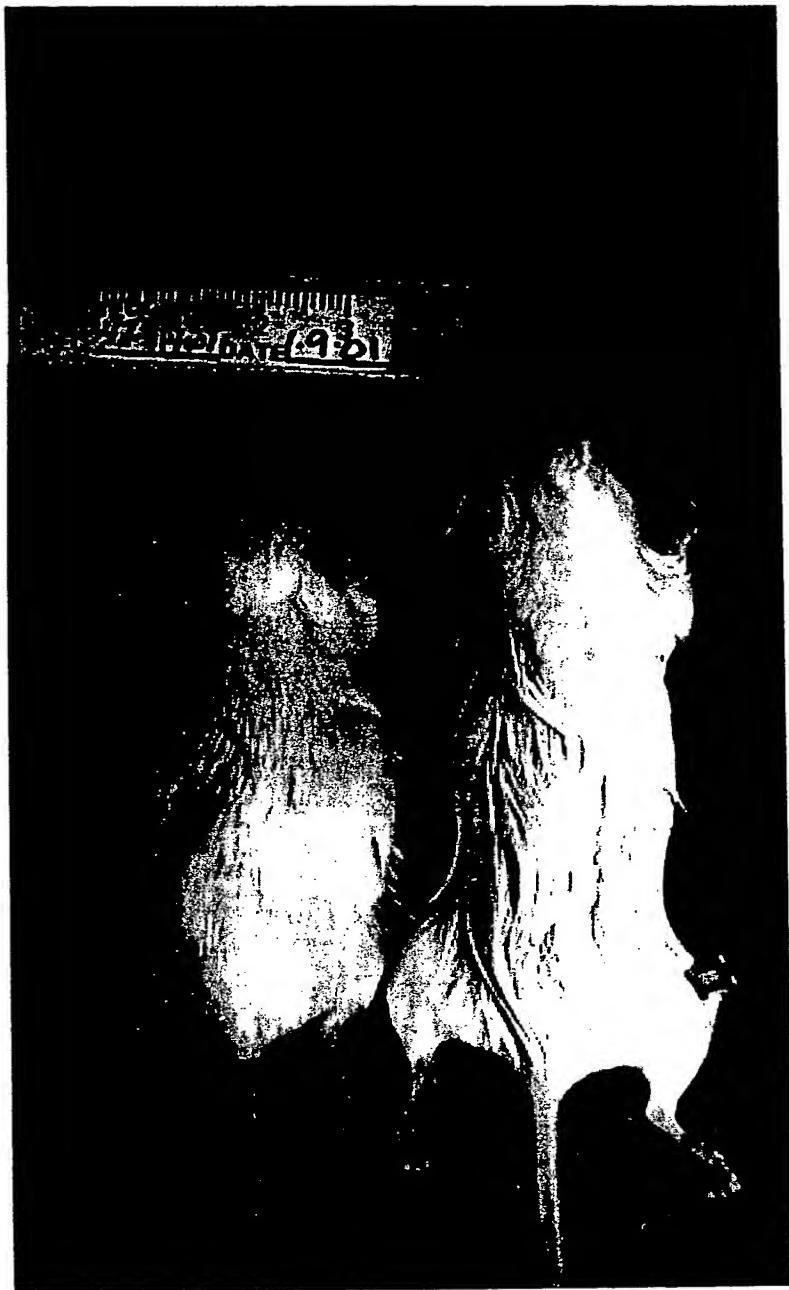


FIG. 55

IL-17E transgenics are jaundiced by 6 weeks of age



TG

WT

FIG. 56

mIL-17E transgenics have elevated total bilirubin and liver enzymes

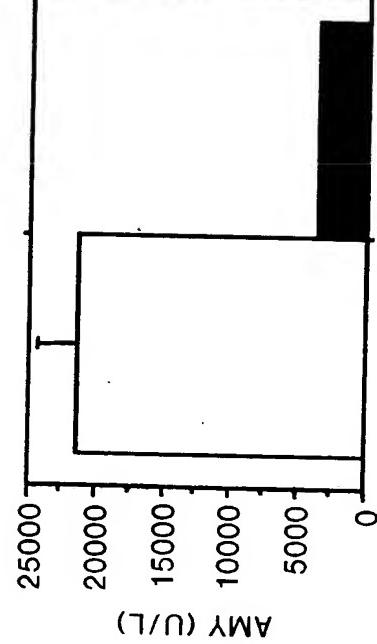
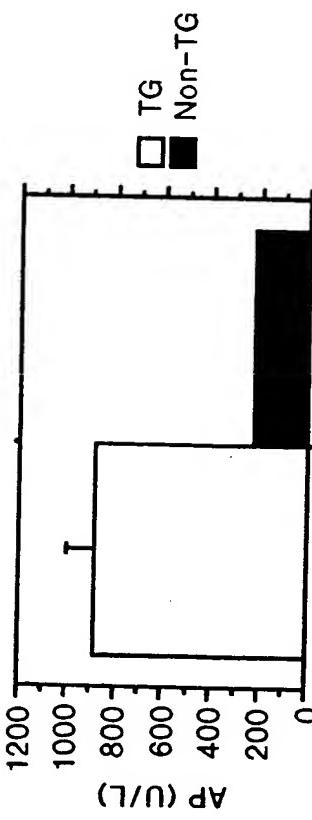
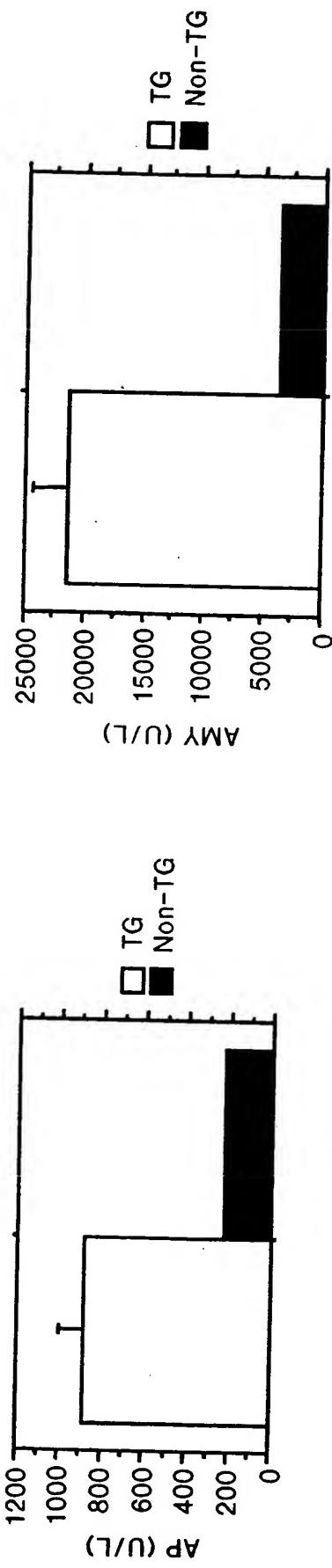
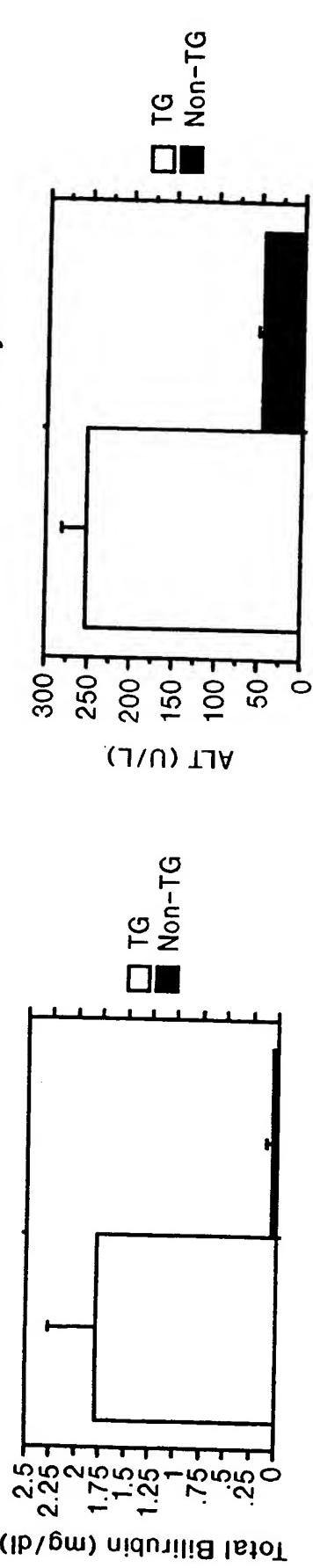


FIG. 57

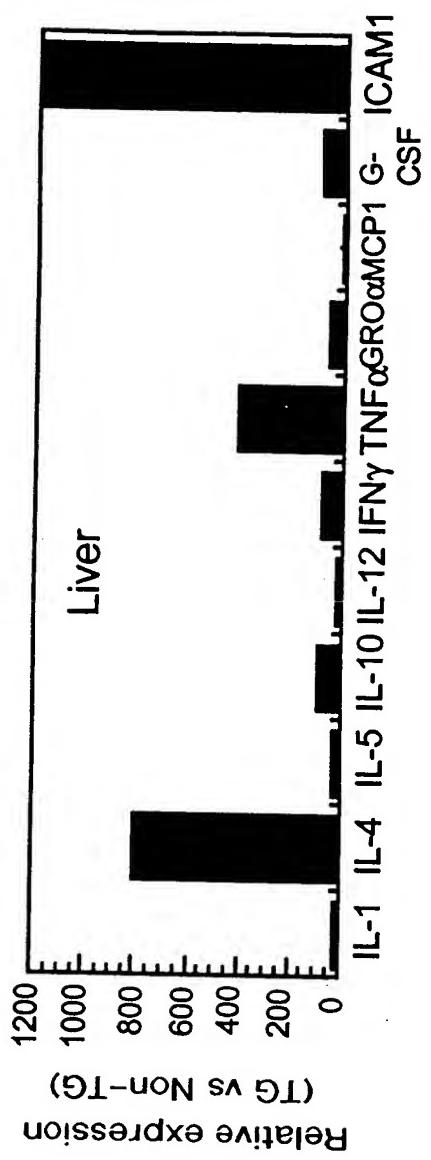


FIG. 58A

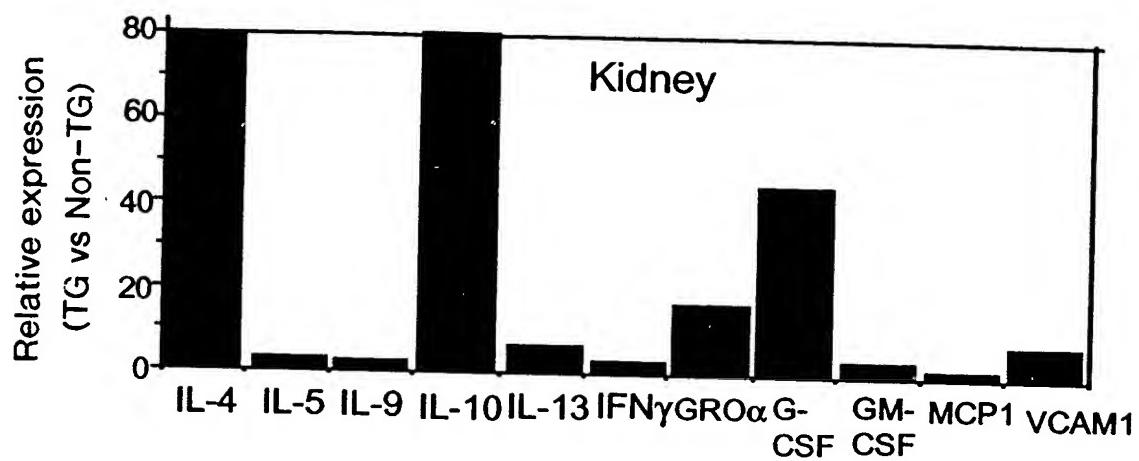


FIG. 58B

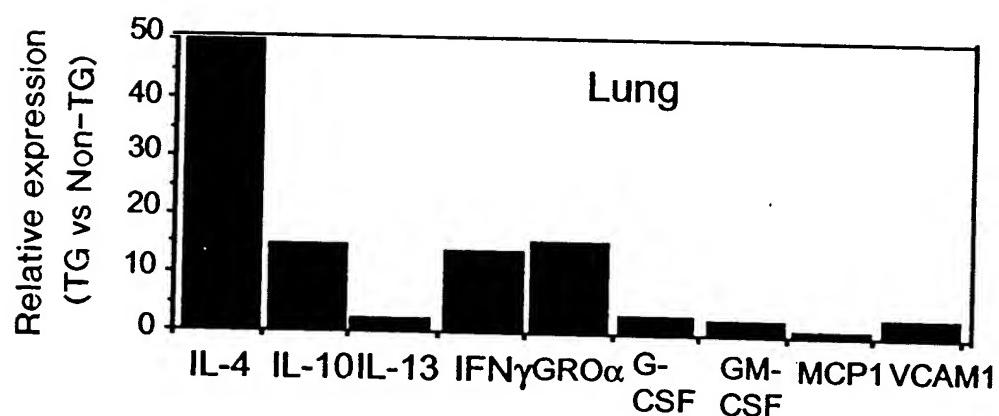


FIG. 58C

Gene profiling of IL-17E transgenics (Taqman)

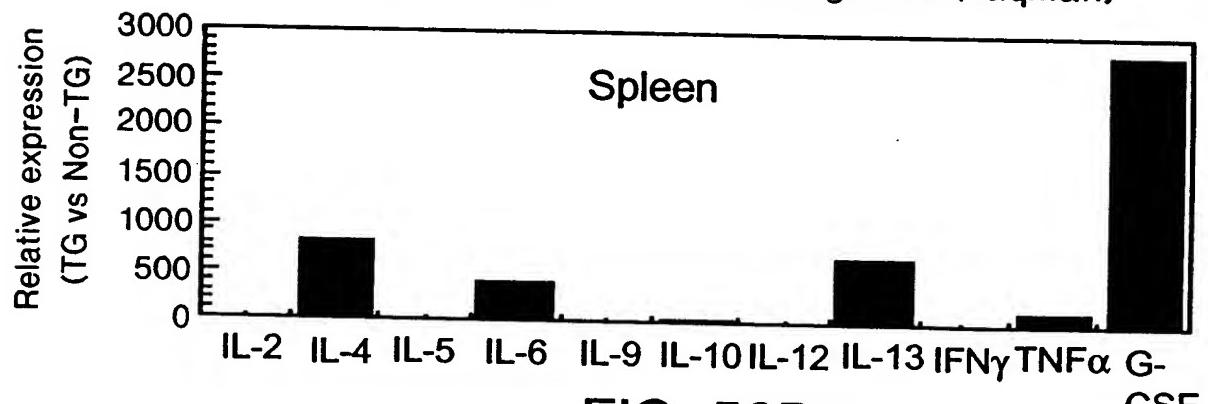


FIG. 58D

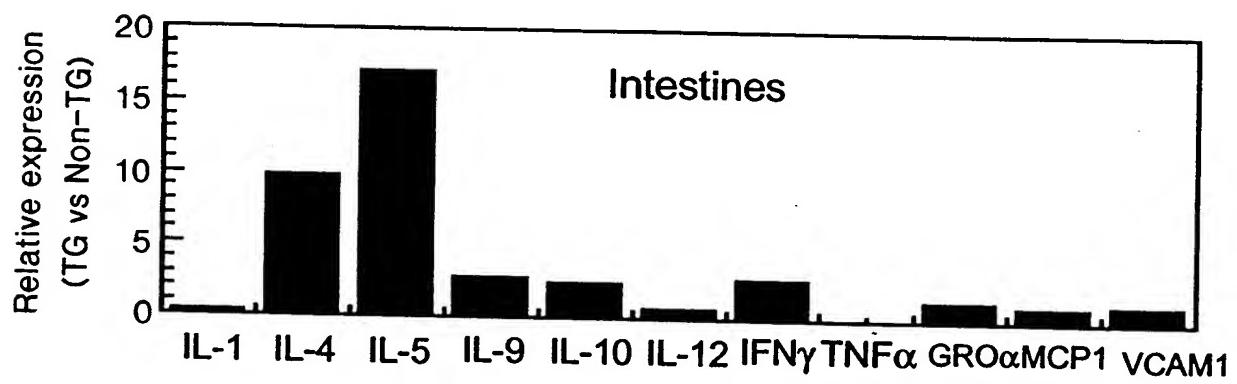


FIG. 58E

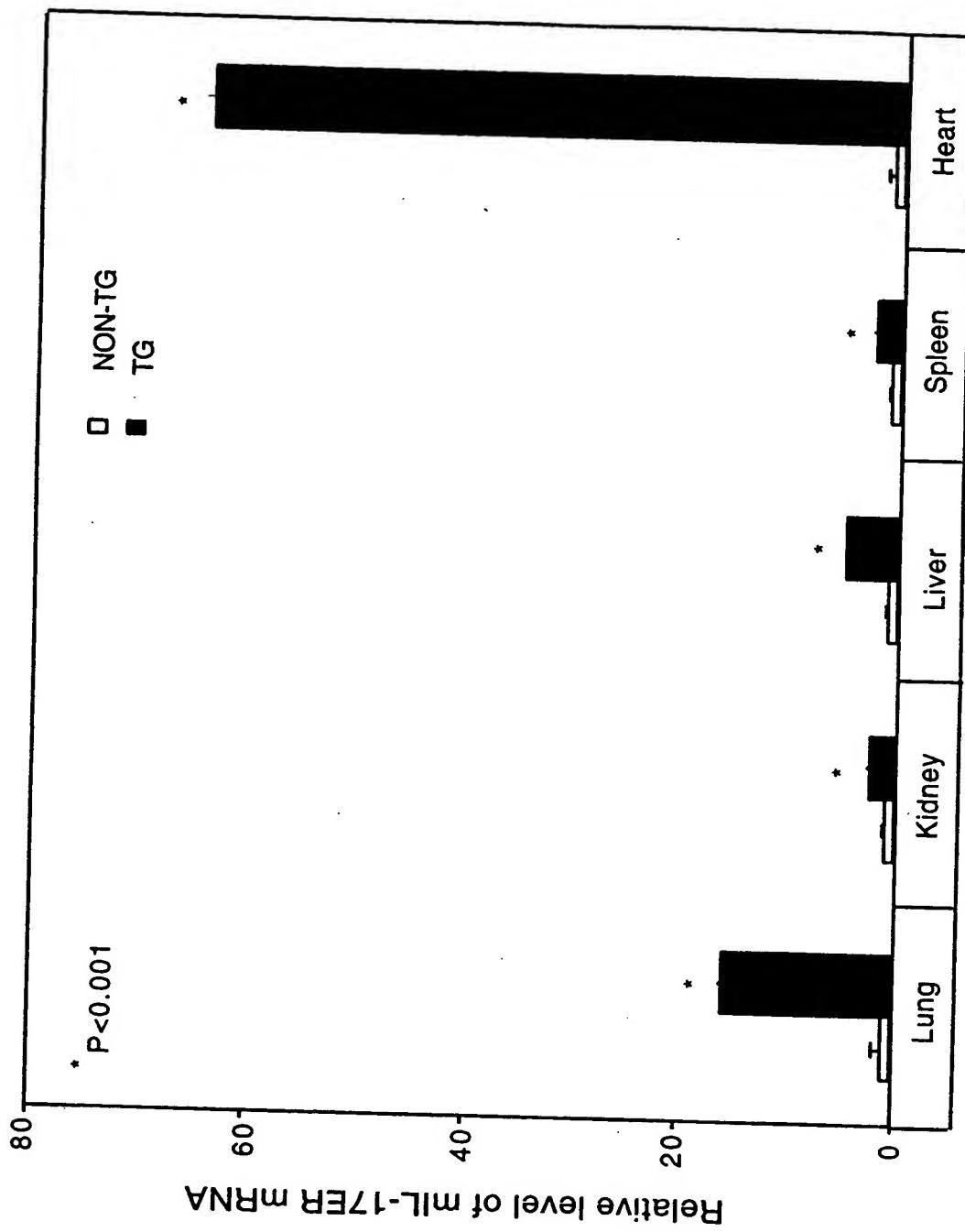


FIG. 59

**Elevated serum IL-5, IL-13 and TNF α
in mIL-17E transgenics**

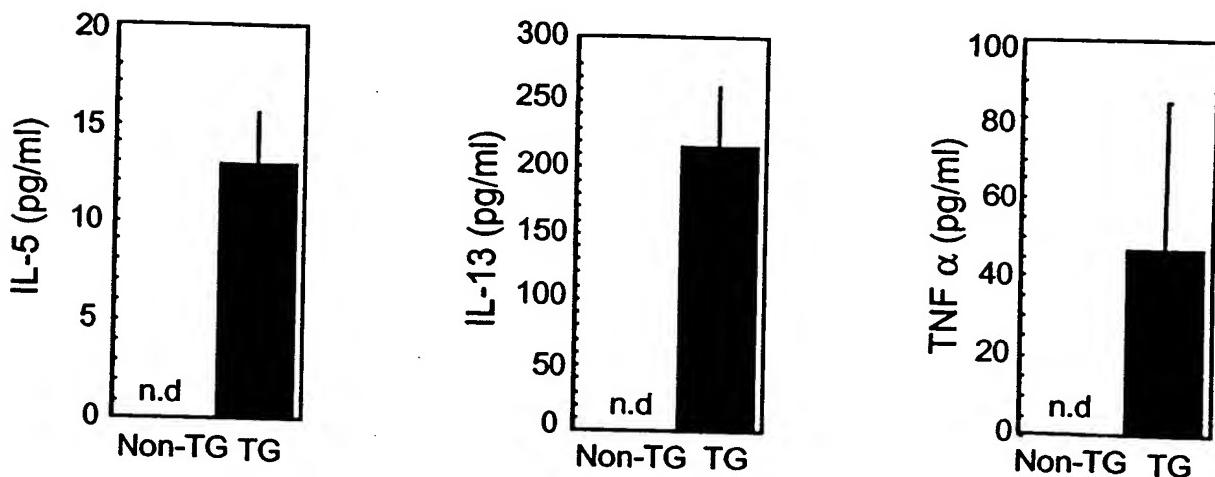


FIG. 60

**Serum IgE and IgG1, but not IgG2a is elevated
in mIL-17E transgenics**

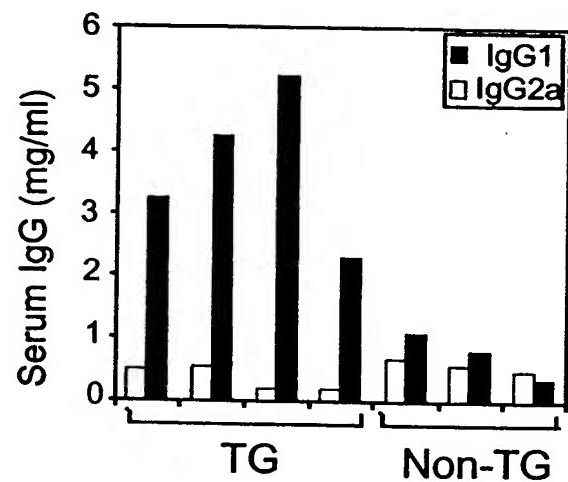
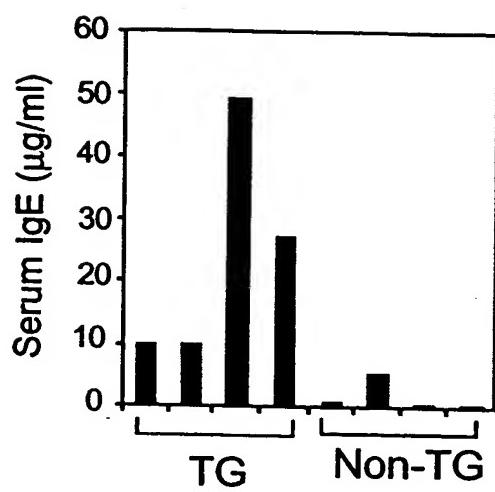


FIG. 61

**Neutrophilia in mIL-17E transgenics
(8 wks, PBMC by FACS)**

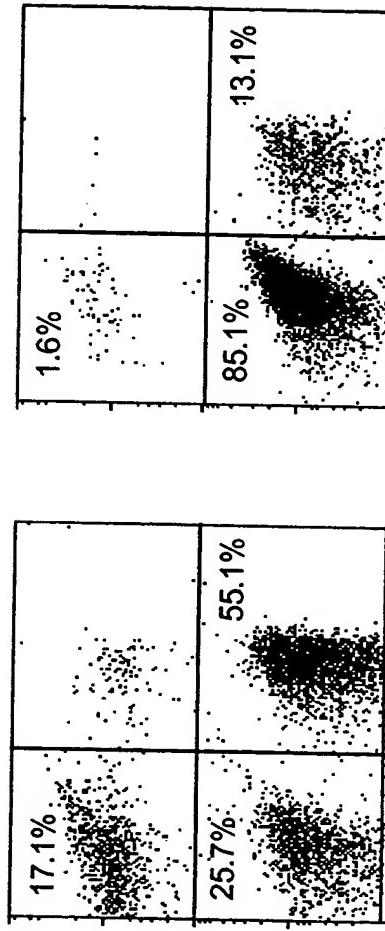


FIG. 62A
Non-TG FITC CD3 TG

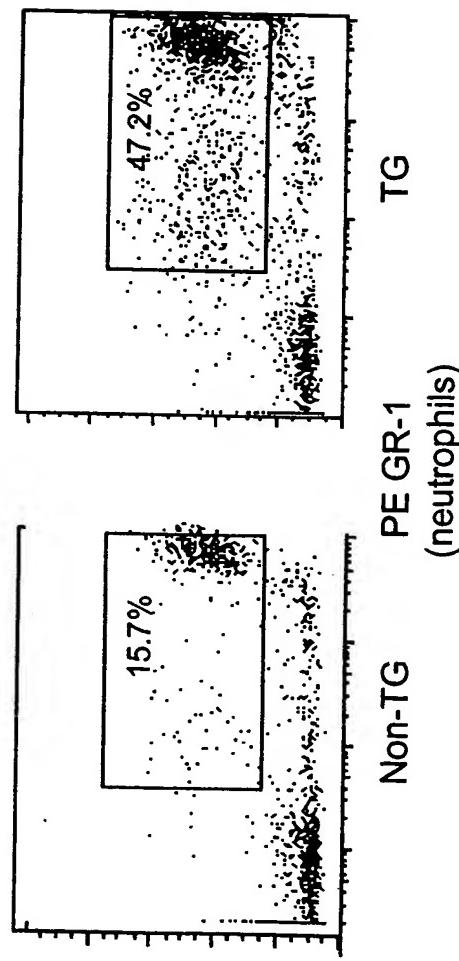


FIG. 62B
Non-TG PE GR-1
(neutrophils) TG

Neutrophilia and eosinophilia in mIL-17E transgenics (hematology)

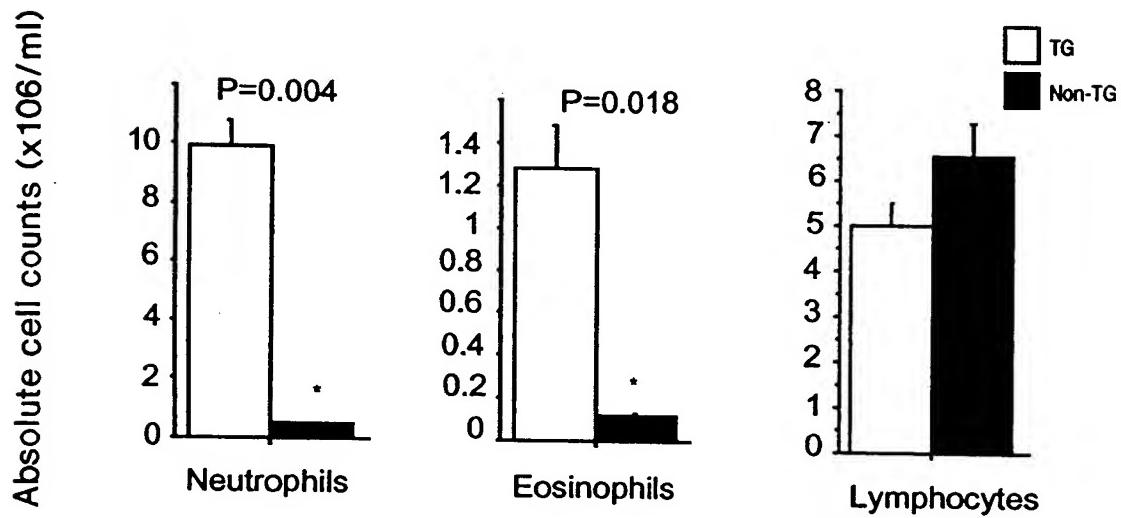


FIG. 63

**G-CSF is elevated in
mIL-17E transgenics**

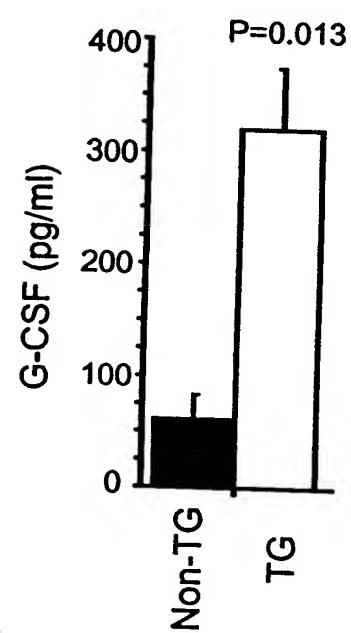
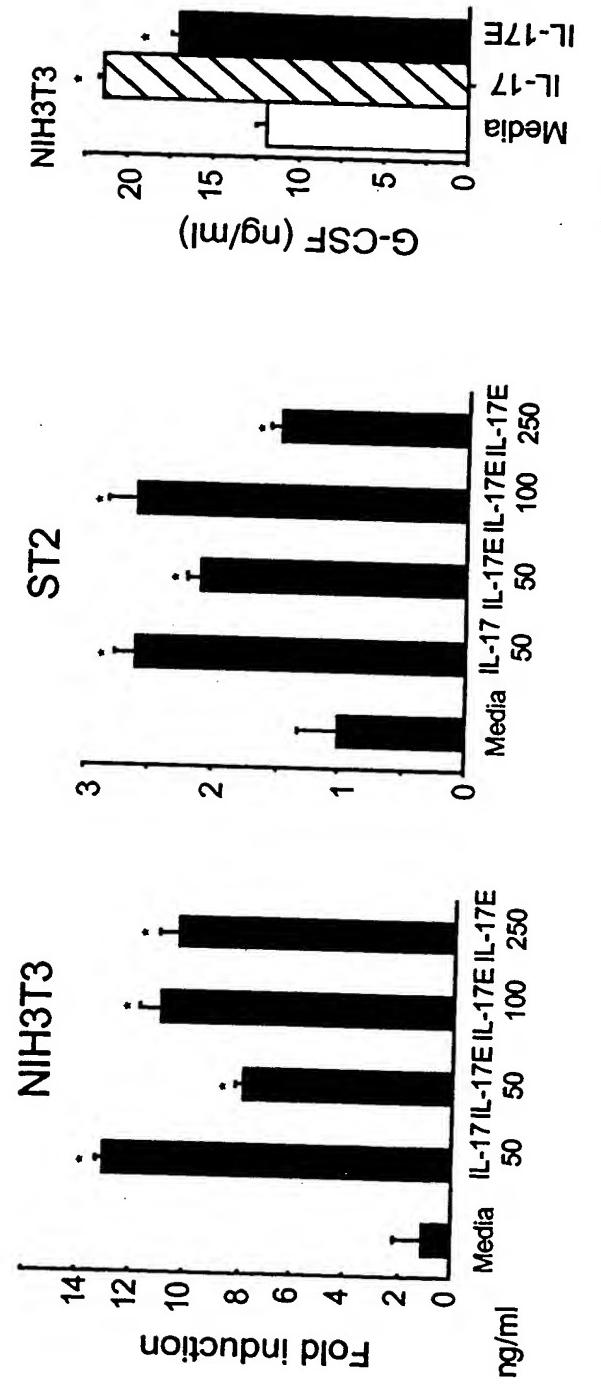


FIG. 64

IL-17E induces production of G-CSF in vitro



* $P < 0.05$

FIG. 65

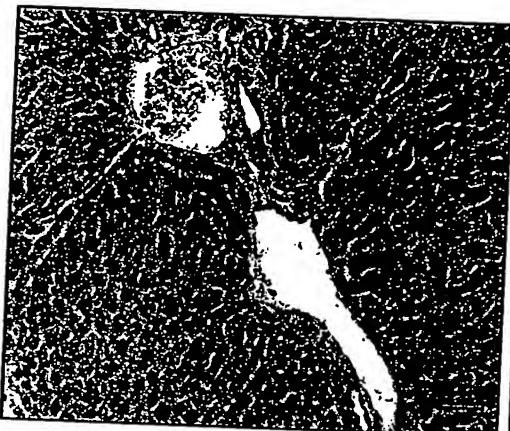


FIG. 66A

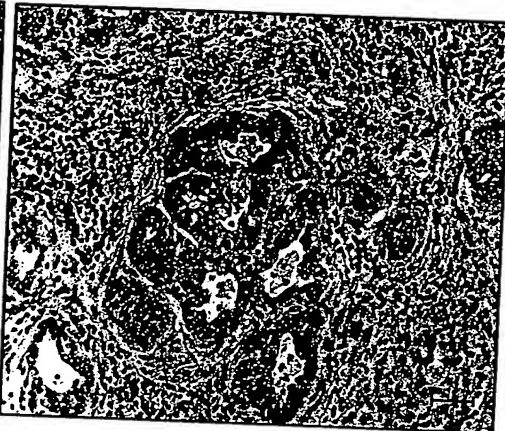


FIG. 66B

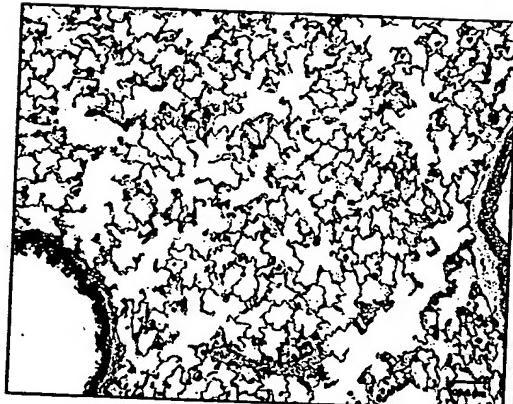


FIG. 66C

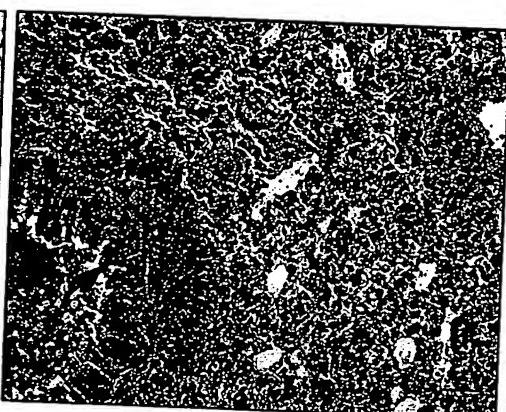


FIG. 66D